

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 22.2289 Seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179a-2
Perfect score: 341
Sequence: 1 KDRPFCBLPDTGRCRVRF.....CEGNANNTKRCBSTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: SP_Archaea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341	100.0	83	13	Q90WAI pseudonaja
2	322	94.4	83	13	Q90WAO pseudonaja
3	245	71.8	83	13	Q90W99 pseudonaja
4	241	70.7	83	13	Q90W98 pseudonaja
5	241	70.7	83	13	Q90W96 pseudonaja
6	226	66.3	83	13	Q90W97 pseudonaja
7	202	59.2	88	13	Q8AY43 bungarus ca
8	198	58.1	58	13	Q9TW98 pseudonaja
9	190	55.7	59	13	Q9TW98 pseudonaja
10	189	55.4	88	13	Q8AY42 bungarus ca
11	187.5	55.0	76	5	Q8T719 bombyx mori
12	185	54.3	58	5	Q9TW90 anemonia su
13	185	54.3	86	5	Q9GP15 ixodes ric
14	183	53.7	88	11	Q8AY41 bungarus ca
15	183	53.7	230	11	Q8CP99 rattus norv
16	182.5	53.5	80	5	Q8T387 araneus ven

17	181	53.1	984	5	Q9GON2 calliacis
18	181	53.1	984	5	Q9GON1 calliacis
19	178	52.2	142	5	Q8WP12 boophilus m
20	175	51.3	142	5	Q8WP13 boophilus m
21	172	50.4	759	5	Q8TR91 ancylostoma
22	171.5	50.3	57	5	Q8MTR6 haemobio
23	171	50.1	113	5	Q9V508 drosophila
24	169	49.6	235	11	Q8CI80 mus musculu
25	169	49.6	235	11	Q8BSB7 canis famil
26	169	49.6	396	6	Q28874 canis famil
27	168	49.3	79	13	Q9I351 dendroaspis
28	163	47.8	132	5	Q9VGT9 drosophila
29	163	47.8	195	11	Q9D8Q8 mus musculu
30	162	47.5	1572	5	Q44938 haemochus
31	161	47.2	576	4	Q8TEU8 homo sapien
32	160	46.9	548	4	Q96N28 homo sapien
33	160	46.9	979	4	Q8N421 homo sapien
34	160	46.9	3198	5	Q9U8G8 manduca sex
35	158	46.3	82	5	Q8MVB4 ixodes ric
36	157	46.0	222	11	Q8R0S6 mus musculu
37	157	46.0	222	11	Q8R0S6 mus musculu
38	156.5	45.9	76	5	Q96S88 gallieria me
39	156	45.7	137	6	Q9BD10 dracopila
40	155	45.5	738	13	Q90W28 dracopila
41	154	45.2	461	5	Q9S622 drosophila
42	154	45.2	747	13	Q9I963 xenopus. ap
43	154	45.2	763	5	Q9XZD0 drosophila
44	153	44.9	133	6	Q8HZ45 papio papio
45	152	44.6	169	6	Q9NOX7 bos taurus

ALIGNMENTS

RESULT 1

ID	Q90WAI	PRELIMINARY;	PRT;	83 AA.
AC	Q90WAI			
DT	01-DEC-2001 (TEMBLrel. 19, Created)			
DT	01-DEC-2001 (TEMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TEMBLrel. 23, Last annotation update)			
DE	Textillina.			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Whittaker A.N., Gaffney P.J., Sorokina I.N., Filipovich I.V.,			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF402324; AAK95519.1; -			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI.1.			
DR	ProDom; PD000222; Kunitz_BPTI.1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.			
KW	Protease inhibitor; Serine protease inhibitor.			
SQ	SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;			
Query Match	100.0%;	Score 341;	DB 13;	Length 83;
Best Local Similarity	100.0%;	Pred. No. 1.3e-36;		
Matches 59;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 2

Q90W99 AC O90W99 PRELIMINARY; PRT; 83 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9179 MW; 678589AD27175930 CRC64;

Query Match 94.4%; Score 322; DB 13; Length 83;
 Best Local Similarity 93.2%; Pred. No. 3.7e-34;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 3

Q90W99 AC O90W99 PRELIMINARY; PRT; 83 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF402326; AAK95521.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9158 MW; 368E82487ACFB61 CRC64;

Query Match 71.8%; Score 245; DB 13; Length 83;
 Best Local Similarity 67.8%; Pred. No. 3.6e-24;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 4

Q90W98 AC O90W98 PRELIMINARY; PRT; 83 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF402327; AAK95522.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 8983 MW; 3F28548146548A9B CRC64;

Query Match 70.7%; Score 241; DB 13; Length 83;
 Best Local Similarity 71.2%; Pred. No. 1.2e-23;
 Matches 42; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 5

Q90W96 AC O90W96 PRELIMINARY; PRT; 83 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RT "Plasma in inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RA Filippovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402328; AAK95523.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.1.
DR ProDom; PD000222; Kunitz_BPTI.1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR KX Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9060 MW; A66DF2692864C58E CRC64;

Query Match 70.7%; Score 241; DB 13; Length 83;
Best Local Similarity 71.2%; Pred. No. 1.2e-23;
Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 KDRPFCBLPADGPCVRPPSPFYNPDEKKCLEFIYGGCGGNANFTTKECESTCA 59
DB 25 KDRPFCBLPADGPCVDPPGAFHYSRHEHCIFITGGCGGNANFTTKECESTCA 83

RESULT 6
O90W97 PRELIMINARY; PRT; 83 AA.
AC O90W97;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-MAR-2003 (Tremblrel. 19, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RT "Plasma in inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RA Filippovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402328; AAK95523.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.1.
DR ProDom; PD000222; Kunitz_BPTI.1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KX Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;

Query Match 66.3%; Score 226; DB 13; Length 83;
Best Local Similarity 67.8%; Pred. No. 1e-21;
Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPFCBLPADGPCVRPPSPFYNPDEKKCLEFIYGGCGGNANFTTKECESTCA 59
DB 25 KDRPFCBLPADGPCVDPPGAFHYSRHEHCIFITGGCGGNANFTTKECESTCA 83

RESULT 7
O8AY43 PRELIMINARY; PRT; 88 AA.
AC O8AY43;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Kunitz inhibitor a (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057886; AAL30068.1;
FT NON_TER 1 1
SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 59.2%; Score 202; DB 13; Length 88;
Best Local Similarity 56.9%; Pred. No. 1.4e-18;
Matches 33; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 KDRPFCBLPADGPCVRPPSPFYNPDEKKCLEFIYGGCGGNANFTTKECESTCA 58
DB 30 KDRPFCBLPADGPCVRPPSPFYNPDEKKCLEFIYGGCGGNANFTTKECESTCA 87

RESULT 8
O9TW99 PRELIMINARY; PRT; 58 AA.
AC O9TW99;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE KALICUDINE 2, ASK2.
OS Anemonea sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymphaeae; Actinidae; Anemonea.
OX NCBI_TaxID=6108;
RN
[1]
RN SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemane E., Moinier D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicudines and kalieptins. Two different classes of sea anemone
RT toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126 (1995).
DR HSSP; P12111; 2KNT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI.1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

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KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; F102E71682F1A55C CRC64;

Query Match 58.1%; Score 198; DB 5; Length 58;
Best Local Similarity 62.7%; Pred. No. 3.1e-18;
Matches 32; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTC 57
Db 5 CLPMDVGRCAARHPFRYYNLSRRCEKFTYGGCGGNANNFITKECEKVC 55

RESULT 9

Q9TWFG PRELIMINARY; PRT; 59 AA.

AC O9TWFG
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE KALICUDINE 3, ASKC3.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.

RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemaire E., Moirier D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicudines and kalieptine. Two different classes of sea anemone
toxins for voltage sensitive K⁺ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).

DR HSP; P31713; ISHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394DA5 CRC64;

Query Match 55.7%; Score 190; DB 5; Length 59;
Best Local Similarity 62.7%; Pred. No. 3.4e-17;
Matches 32; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTC 57
Db 5 CELPKVGRCAARHPFRYYNLSRRCEKFTYGGCGGNANNFITKECEKVC 55

RESULT 10

Q8AY42 PRELIMINARY; PRT; 88 AA.

AC O8AY42
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kunitz inhibitor b (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
RA Test I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057887; AAL30069.1; -.
FT NON_TER 1 1

SQ SEQUENCE 88 AA; 9391 MW; 71P9F57D36E7A652 CRC64;

Query Match 55.4%; Score 189; DB 13; Length 88;
Best Local Similarity 54.4%; Pred. No. 6.9e-17;
Matches 31; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPFCLEPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTC 57
Db 30 KDRKFCVPRPPEPCRCANVAFYNNPRLRKCIEFTYGGCGGNANNFSGGCKRAC 86

RESULT 11

Q8T7L9 PRELIMINARY; PRT; 76 AA.

AC Q8T7L9
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
GN Spil.

OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditypsia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21873253; PubMed=11881808;
RA Nirmala X., Mita K., Vanistree V., Zurovec M., Sehgal F.;
RT "Identification of four small molecular mass proteins in the silk of
Bombyx mori.";
RL Insect Mol. Biol. 10:437-445(2001).
DR EMBL; AF352583; AAL63944.1; -.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 76 AA; 8445 MW; AA3F97D373535A3B CRC64;

Query Match 55.0%; Score 187.5; DB 5; Length 76;
Best Local Similarity 61.1%; Pred. No. 9.4e-17;
Matches 33; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

Qy 4 PDFCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTC 57
Db 23 PD-CLPDKTGPCCKGSPFRVAYDSSEDKCVFITYGGCGGNANNFETIECEAAC 75

RESULT 12

Q9TWG0 PRELIMINARY; PRT; 58 AA.

AC Q9TWG0
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE KALICUDINE 1, ASKC1.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.

RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemaire E., Moirier D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicudines and kalieptine. Two different classes of sea anemone
toxins for voltage sensitive K⁺ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P10646; IADZ.
DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI, 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI, 1.
 DR SMART; SM00131; KU, 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1, 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2, 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 58 AA; 6691 MW; 253806896B4BDCD CRC64;

Query Match 54.3%; Score 185; DB 5; Length 58;
 Best Local Similarity 60.8%; Pred. No. 1.5e-16;
 Matches 31; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTC 57
 Db 5 CLPMDVGRCAHPRYYNSSSRCKRFTYGGCGGNANNFITKECEKVC 55

RESULT 13

ID O9GP15 PRELIMINARY; PRT; 86 AA.
 AC O9GP15;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE Hypothetical 9.7 kDa protein.
 OS Ixodes ricinus (castor bean tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
 OX NCBI_TaxID=34613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Lebouille G., Rochez C., Louahed J., Rutti B., Brosseau M., Bollen A.,
 RA Godfroid B.;
 RT "Isolation of Ixodes ricinus salivary gland mRNAs encoding factors
 RT induced during the blood feeding process."
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ169641; CAB55816.1; -
 DR HSSP; P12111; IKRT.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI, 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI, 1.
 DR SMART; SM00131; KU, 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1, 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2, 1.
 KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 86 AA; 9727 MW; 9473B17974A055F0 CRC64;

Query Match 54.3%; Score 185; DB 5; Length 86;
 Best Local Similarity 52.5%; Pred. No. 2.2e-16;
 Matches 31; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTCA 59
 Db 25 KGRPAKCLPDDGFCRAKIPSYIFDRKTKCKEPMYGGCGGNANNFENITTCQECNA 83

RESULT 14

ID O8AY41 PRELIMINARY; PRT; 88 AA.
 AC O8AY41;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Kunitz inhibitor c (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057888; AAJ30070.1; -
 FT NON_TER
 SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;

Query Match 53.7%; Score 183; DB 13; Length 88;
 Best Local Similarity 56.9%; Pred. No. 4.2e-16;
 Matches 33; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTCA 58
 Db 30 KNRPFCLNLPBPRCAIVRAFYNNRLKRCLEFPYGGCGGNANNFITIDEQRTCA 87

RESULT 15

ID O8CF99 PRELIMINARY; PRT; 230 AA.
 AC O8CF99;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Tissue factor pathway inhibitor-2 precursor.
 GN TPPI-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Placenta;
 RA MEDLINE=2218372; PubMed=12195712;
 RA Hsaka T., Kistel W., Rosenbaum U.;
 RT "CDNA cloning and tissue distribution of the rat ortholog of tissue
 RT factor pathway inhibitor-2."
 RL Thromb. Haemost. 88:356-357(2002).
 DR EMBL; AJ428954; CAD22046.1; -
 KW Signal.
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 230 AA; 26157 MW; 07CD5B9F7D43ED9 CRC64;

Query Match 53.7%; Score 183; DB 11; Length 230;
 Best Local Similarity 56.6%; Pred. No. 1.1e-15;
 Matches 30; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 5 DFCPLPADTGPCRVPRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTC 57
 Db 34 EICLPDMDGFCALIKFYIDRDQCKRRKRYGGCGGNANNFHKKICERTC 86

Search completed: January 23, 2004, 10:27:15
 Job time : 24.289 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 28.4613 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179a-2

Sequence: 1 KDRPFCFELPADTGPCRVRP.....CEGNANPITRECESTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	341	100.0	59 21	AAV15138 Txln 1 Plasmin inh
2	341	100.0	83 21	AAV15145 Proform of Txln 1
3	334	97.9	60 21	AAV15153 Plasmin inhibitor
4	322	94.4	59 21	AAV15139 Proform of Txln 2
5	322	94.4	83 21	AAV15146 Plasmin inhibitor
6	298	87.4	60 21	AAV15154 Txln 3 Plasmin inh
7	245	71.8	59 21	AAV15140 Proform of Txln 3
8	245	71.8	83 21	AAV15147 Txln 6 Plasmin inh
9	227	66.6	59 21	AAV15143

10	227	66.6	83 21	AAV15150
11	226	66.3	59 21	AAV15142
12	226	66.0	83 21	AAV15149
13	225	66.0	59 21	AAV15141
14	225	66.0	83 21	AAV15148
15	221	64.8	58 17	AAV15146
16	201	58.9	58 16	AAV15142
17	196	57.5	58 16	AAV15146
18	192	56.3	58 16	AAV15142
19	189	55.4	58 16	AAV15146
20	185	54.3	86 22	AAV15140
21	185	54.3	124 18	AAV15142
22	185	54.3	144 18	AAV15142
23	184	54.0	58 17	AAV15149
24	183	53.7	55 18	AAV15141
25	183	53.7	60 21	AAV15151
26	183	53.7	124 18	AAV15142
27	183	53.7	144 18	AAV15142
28	183	53.7	145 18	AAV15142
29	183	53.7	165 18	AAV15142
30	182	53.4	58 17	AAV15142
31	182	53.4	58 17	AAV15142
32	181	53.1	58 13	AAV15142
33	181	53.1	58 17	AAV15142
34	181	53.1	58 17	AAV15142
35	180	52.8	58 13	AAV15142
36	180	52.8	58 17	AAV15142
37	180	52.8	58 17	AAV15142
38	179	52.5	58 16	AAV15142
39	179	52.5	58 16	AAV15142
40	177	51.9	58 17	AAV15142
41	176	51.6	58 17	AAV15142
42	175	51.3	58 13	AAV15142
43	175	51.3	58 16	AAV15142
44	175	51.3	58 17	AAV15142
45	174	51.0	58 16	AAV15142

ALIGNMENTS

RESULT 1
AAV15138
ID AAV15138 standard; Protein; 59 AA.
XX AAV15138;
XX
DT 07-FEB-2000 (first entry)
XX
DE Txln 1 Plasmin inhibitor protein.
XX
XX Textilin protein; Txln 1, plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytoskeletal activity; homology; specificity; Apoptin;
XX Talocoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; chromobiosis.
XX
XX Pseudonaja textilis textilis.
XX
XX WO9558569-A1-7
XX
XX PD 18-NOV-1999.
XX
XX PF 07-MAY-1999; 99WO-AU00343.
XX
XX PR 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU) UNIV QUEBENS/LAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC-) MASC P P.
XX (LAVI/) LAVIN M F.

Proform of Txln 6
Txln 5 Plasmin inh
Proform of Txln 5
Txln 4 Plasmin inh
Proform of Txln 4
Apoptin-like Kun
Human LACI-K2 deri
Human collagen alp
Human TPPI-2 domai
Human LACI-K3 deri
I. ricinus salivar
New protease inhib
SUC2-Bp7-d21-RPDP-
Genetically engine
RPDP-Kunitz domain
Plasmin inhibitor
New protease inhib
SUC2-Bp1-d21-RPDP-
Novel protease inh
Elastase inhibitor
Genetically engine
Human neutrophil e
Genetically engine
Genetically engine
Human TPPI-2 domai
Human LACI-K1 deri
Genetically engine
Human neutrophil e
HKT B9 KUDOM deriv
Genetically engine
Human LACI-K1 deri

PA (GAF/) GAFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX
 DR WPI: 2000-039073/03.
 DR N-PSDB; AA229017.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 8a; Page 68; 112pp; English.
 XX
 CC The present sequence is the Textilinin protein, Txln 1, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 458 and
 CC 588 homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 59 AA;
 XX
 Query Match 100.0%; Score 341; DB 21; Length 59;
 Best Local Similarity 100.0%; Pred. No. 8.6e-34;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANPFTKCESTCAA 59
 Db 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANPFTKCESTCAA 59
 XX
 RESULT 2
 ID AAY15145 standard; Protein; 83 AA.
 AC AAY15145;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Proform of Txln 1 protein.
 XX
 KW Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KW haematopoietic; cytostatic activity; homology; specificity; control;
 KW Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 KW
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= leader_peptide
 FT 25..83
 FT /label= Txln-1 protein
 FT /note= "Textilinin-1"
 FT
 XX
 XX WO958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99MO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 XX
 XX (UYOU) UNIV QUEENSLAND.
 PA

PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX
 DR WPI: 2000-039073/03.
 DR N-PSDB; AA229024.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 40a; Page 71; 112pp; English.
 XX
 CC The present sequence is the proform of the Textilinin protein, Txln 1,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 458 and
 CC 588 homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 83 AA;
 XX
 Query Match 100.0%; Score 341; DB 21; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.2e-33;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANPFTKCESTCAA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANPFTKCESTCAA 83
 XX
 RESULT 3
 ID AAY15153 standard; Protein; 60 AA.
 AC AAY15153;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.
 XX
 KW Textilinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; homology; specificity; enzyme;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW inhibitory efficiency; reduced propensity; thrombosis.
 KW
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 24
 FT /note= "encoded by TTG"
 FT MISC-difference 47
 FT /note= "encoded by GAT"
 FT MISC-difference 49
 FT /note= "encoded by ATG"
 FT
 XX
 XX WO958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99MO-AU00343.
 XX
 XX

```

PR 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASC P P.
PA (LAVI/) LAVIN M F.
PA (GAF/) GAFFNEY P J.
PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
XX
XX MPI; 2000-039073/03.
DR N-PSDB; AA229047.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
PS Disclosure; Fig 6; 112pp; English.
XX
XX The present amino acid sequence is the Txln 1, Textillin protein
CC encoded by the partial cDNA sequence. It is a single stage competitive
CC inhibitor of plasmin. It is isolated from the Australian brown snake,
CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
CC low inhibitory efficiency that can transiently affect the delicate
CC balance between enzymes and inhibitors of the fibrinolytic system,
CC controlling the fluidity of blood. The plasmin inhibitors are useful for
CC alleviating blood loss, following major surgery or trauma. Conjugates of
CC the plasmin inhibitor and an anti-fibrin antibody are useful as
CC anti-tumour agents. They have reduced propensity to cause thrombosis.
XX
SQ Sequence 60 AA;
XX
XX Query Match 97.9%; Score 334; DB 21; Length 60;
XX Best Local Similarity 96.6%; Pred. No. 6.2e-33;
XX Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
Db |||||
2 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCGS 60
XX
XX RESULT 4
XX ID AAY15139 standard; Protein; 59 AA.
XX
XX AAY15139;
XX
XX 07-FEB-2000 (first entry)
XX
XX Txln 2 Plasmin inhibitor protein.
XX
XX Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytosolic activity; homology; specificity; Aprotinin;
XX Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX OS MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAF/) GAFFNEY P J.

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XX
XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
PI
XX MPI; 2000-039073/03.
DR N-PSDB; AA229018.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
PS Claim 8b; Page 69; 112pp; English.
XX
XX The present sequence is the Textillin protein. Txln 2 that is a
CC single stage competitive inhibitor of plasmin. It is isolated from the
CC Australian brown snake, Pseudonaja textilis textilis. It has six
CC conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytosolic activity. Txln 2 has 43% and
CC 55% homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
CC (TAC), respectively. Txln has high specificity for plasmin and low
CC inhibitory efficiency, that can transiently affect the delicate balance
CC between enzymes and inhibitors of the fibrinolytic system, controlling
CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
CC blood loss, following major surgery or trauma. Conjugates of the plasmin
CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
CC They have reduced propensity to cause thrombosis.
XX
SQ Sequence 59 AA;
XX
XX Query Match 94.4%; Score 322; DB 21; Length 59;
XX Best Local Similarity 93.2%; Pred. No. 1.7e-31;
XX Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
Db |||||
1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
XX
XX RESULT 5
XX ID AAY15146 standard; Protein; 83 AA.
XX
XX AAY15146;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 2 protein.
XX
XX Textillin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
XX haematopoietic; cytosolic activity; homology; specificity; control;
XX Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX OS MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

```

PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX
 DR WPI: 2000-039073/03.
 DR N-PSDB: AAZ29025.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PS
 PS Claim 40b; Page 71; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillin protein, Txln 2,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 2 has 43* and
 CC 5* homology with Aprotinin and Taticotin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 83 AA;
 XX
 Query Match 94.4%; Score 322; DB 21; Length 83;
 Best Local Similarity 93.2%; Pred. No. 2.5e-31;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KDRPFCPLPADTGPCRVRRPSPFYNNPDEKCLBFIYGGCEGNANFFITKECESTCA 59
 Db 25 KDRPFCPLPADTGPCRVRRPSPFYNNPDEKCLBFIYGGCEGNANFFITKECESTCA 83
 XX
 RESULT 6
 AAY1514
 ID AAY1514 standard; Protein; 60 AA.
 XX
 AC AAY1514;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
 XX
 KM Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; homology; enzyme;
 KM fluidity of blood; aleviate; blood loss; major surgery; trauma;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM inhibitory efficiency; reduced propensity; thrombosis.
 KM
 XX
 OS Pseudonaja textilis textilis.
 XX
 Key Location/Qualifiers
 FH Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 45
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"
 FT Misc-difference 59
 FT /note= "encoded by CCN"
 XX
 XX W09958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.

XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX
 DR WPI: 2000-039073/03.
 DR N-PSDB: AAZ29048.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PS
 PS Disclosure; Fig 7; 112pp; English.
 XX
 CC The present amino acid sequence is the Txln 2, Textillin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 60 AA;
 XX
 Query Match 87.4%; Score 298; DB 21; Length 60;
 Best Local Similarity 89.5%; Pred. No. 1.4e-28;
 Matches 51; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KDRPFCPLPADTGPCRVRRPSPFYNNPDEKCLBFIYGGCEGNANFFITKECESTC 57
 Db 2 KDRPFCPLPADTGPCRVRRPSPFYNNPDEKCLBFIYGGCEGNANFFITKECESTC 58
 XX
 RESULT 7
 AAY15140
 ID AAY15140 standard; Protein; 59 AA.
 XX
 AC AAY15140;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Txln 3 Plasmin inhibitor protein.
 XX
 KM Textillin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; aleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 KM
 XX
 OS Pseudonaja textilis textilis.
 XX
 W09958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.

XX (GAF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229026.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 XX
 PS Claim 40c; Page 72; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillinin protein, Txln 3, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 XX
 Query Match 71.8%; Score 245; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 3.5e-22;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 DB 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 RESULT 8
 AAY15147
 ID AAY15147 standard; Protein; 83 AA.
 XX
 AC AAY15147;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DB Proform of Txln 3 protein.
 XX
 KW Textillinin proform, Txln 3; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_Peptide
 FT Protein 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFFNEY P J.

PA (GAF/) GAFFNEY P J.
 XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229026.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 XX
 PS Claim 40c; Page 72; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillinin protein, Txln 3,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 83 AA;
 XX
 Query Match 71.8%; Score 245; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 5e-22;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 DB 25 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 83
 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 59
 1 KDRPDCFLPADTGPCVRRPFFYNDPEKKCLEFIYGGCGNANNFTTKECESTCA 83
 RESULT 9
 AAY15143
 ID AAY15143 standard; Protein; 59 AA.
 XX
 AC AAY15143;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DB Txln 6 Plasmin inhibitor protein.
 XX
 KW Textillinin protein, Txln 6; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_Peptide
 FT Protein 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229022.

XX N-PSDB; AAZ29029.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor

PT agents -

XX

PS Claim 40f, Page 72, 112pp; English.

XX

CC The present sequence is the proform of the Textilinin protein, Txln 6,

CC that is a single stage competitive inhibitor of plasmin. It is isolated

CC from the Australian brown snake, Pseudonaja textilis textilis. It has

CC six conserved cysteine residues, that endow them great stability. This

CC sequence has haemacopeletic and cyostatic activity. Txln has high

CC specificity for plasmin and low inhibitory efficiency, that can

CC transiently affect the delicate balance between enzymes and inhibitors

CC of the fibrinolytic system, controlling the fluidity of blood. The

CC plasmin inhibitors are useful for alleviating blood loss, following

CC major surgery or trauma. Conjugates of the plasmin inhibitor and an

CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced

CC propensity to cause thrombosis.

XX

XX Sequence 83 AA;

SO

Query Match 66.6%; Score 227; DB 21; Length 83;

Best Local Similarity 67.8%; Pred. No. 7.5e-20;

Matches 40; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 1 KDRPDCFLPADTGPCRVKRPFSFYTNPDEKKCLBFYIGGCGEGNANNITKEBCSTCA 59

DB 25 KDRKFCFLPADIGPMDFTGAHFYSPREHCIEFYIGGCKGNANNNTQECSTCA 83

RESULT 11

AAV15142

ID AAV15142 standard; Protein; 59 AA.

XX

AC AAV15142;

XX

DT 07-FEB-2000 (first entry)

XX

DE Txln 5 Plasmin inhibitor protein.

XX

Textilinin protein; Txln 5; plasmin inhibitor; single stage inhibitor;

KW Australian brown snake; conserved cysteine residue; stability; control;

KW haemacopeletic; cyostatic activity; specificity; inhibitory efficiency;

KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;

KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;

XX reduced propensity; thrombosis.

XX

OS Pseudonaja textilis textilis.

XX

PN WO958569-A1.

XX

PD 18-NOV-1999.

XX

PE 07-MAY-1999; 99WO-AU00343.

XX

PR 11-MAY-1998; 98AU-0003450.

XX

PA (UNBUT) UNIT QUEENSLAND.

PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.

PA (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

PA (GAFF/) GAFFNEY P J.

XX

PI Macci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

XX

DR WPI: 2000-039073/03.

XX

DR N-PSDB; AAZ29021.

XX

PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor

XX agents -

XX

PS Claim 8e, Page 69, 112pp; English.

XX The present sequence is the Textillinin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

SQ Sequence 59 AA;

Query Match 66.3%; Score 226; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 6.9e-20;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPDCLELPADPGPCVRFPSPFYNDPEKKCLEFIVGCGGNANPITKECESTCA 59
 Db 1 KDRPDCLELPADPGSCSDFTGAFHYSTRDRCEIFIVGCGGNANPITKECESTCA 59

RESULT 12

AA15149 standard; Protein; 83 AA.

AA15149;

07-FEB-2000 (first entry)

Proform of Txln 5 protein.

XX Textillinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX reduced propensity; thrombosis.

OS Pseudonaja textilis textilis.

Key Location/Qualifiers

Peptide 1..24 /label= Leader_peptide

Protein 25..83 /label= Txln-5 protein

/note= "Textillinin-5"

MO9958569-A1.

18-NOV-1999.

07-MAY-1999; 99WO-AU00343.

11-MAY-1998; 98AU-0003450.

(UYOU) UNIV QUEENSLAND.

(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

(MASC/) MASC P P.

(LAVI/) LAVIN M F.

(GAF/) GAFFNEY P J.

Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

WPI; 2000-039073/03.

N-PSDB; AA229028.

PS Claim 40e; Page 72; 112pp; English.

XX The present sequence is the proform of the Textillinin protein, Txln 5,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

SQ Sequence 83 AA;

Query Match 66.3%; Score 226; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 9.9e-20;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPDCLELPADPGPCVRFPSPFYNDPEKKCLEFIVGCGGNANPITKECESTCA 59
 Db 25 KDRPDCLELPADPGSCSDFTGAFHYSTRDRCEIFIVGCGGNANPITKECESTCA 83

RESULT 13

AA15141 standard; Protein; 59 AA.

AA15141;

07-FEB-2000 (first entry)

Txln 4 plasmin inhibitor protein.

XX Textillinin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX reduced propensity; thrombosis.

OS Pseudonaja textilis textilis.

Key Location/Qualifiers

Peptide 1..24 /label= Leader_peptide

Protein 25..83 /label= Txln-5 protein

/note= "Textillinin-5"

MO9958569-A1.

18-NOV-1999.

07-MAY-1999; 99WO-AU00343.

11-MAY-1998; 98AU-0003450.

(UYOU) UNIV QUEENSLAND.

(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

(MASC/) MASC P P.

(LAVI/) LAVIN M F.

(GAF/) GAFFNEY P J.

Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

WPI; 2000-039073/03.

N-PSDB; AA229020.

PS Claim 8d; Page 69; 112pp; English.

XX The present sequence is the Textillinin protein, Txln 4, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

SQ Sequence 83 AA;

Query Match 66.3%; Score 226; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 9.9e-20;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPDCLELPADPGPCVRFPSPFYNDPEKKCLEFIVGCGGNANPITKECESTCA 59
 Db 25 KDRPDCLELPADPGSCSDFTGAFHYSTRDRCEIFIVGCGGNANPITKECESTCA 83

RESULT 13

AA15141 standard; Protein; 59 AA.

AA15141;

07-FEB-2000 (first entry)

Txln 4 plasmin inhibitor protein.

XX Textillinin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX reduced propensity; thrombosis.

OS Pseudonaja textilis textilis.

Key Location/Qualifiers

Peptide 1..24 /label= Leader_peptide

Protein 25..83 /label= Txln-5 protein

/note= "Textillinin-5"

MO9958569-A1.

18-NOV-1999.

07-MAY-1999; 99WO-AU00343.

11-MAY-1998; 98AU-0003450.

(UYOU) UNIV QUEENSLAND.

(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

(MASC/) MASC P P.

(LAVI/) LAVIN M F.

(GAF/) GAFFNEY P J.

Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

WPI; 2000-039073/03.

N-PSDB; AA229020.

CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 59 AA;

Query Match 66.0%; Score 225; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 9.1e-20;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGCRCRFRPSFYNNPDEKCKLEPTYGCCGNNANFTKECESTCA 59
 DB 1 KDHPFCFLPADTGCRCRFRPSFYNNPDEKCKLEPTYGCCGNNANFTKECESTCA 59

RESULT 14

AA15148
 ID AA15148 standard; Protein; 83 AA.

AC AA15148;

DT 07-FEB-2000 (first entry)

DE Proform of Txln 4 protein.

XX Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitor efficiency;
 KW fluidity of blood; allergy; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX Key Location/Qualifiers

FT Peptide 1..24
 FT /label= leader_peptide
 FT Protein 25..83
 FT /label= Txln-4 protein
 FT /note= "Textilin-4"

XX MO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASI P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFFNEY P J.

XX Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

XX WPI; 2000-039073/03.

XX N-PSDB; AA220927.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor

XX agents -
 XX Claim 40d; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textilin protein, Txln 4,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has

CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 83 AA;

Query Match 66.0%; Score 225; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 1.3e-19;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGCRCRFRPSFYNNPDEKCKLEPTYGCCGNNANFTKECESTCA 59
 DB 25 KDHPFCFLPADTGCRCRFRPSFYNNPDEKCKLEPTYGCCGNNANFTKECESTCA 83

RESULT 15

AA99146
 ID AA99146 standard; protein; 58 AA.

AC AA99146;

DT 12-FEB-1997 (first entry)

DE Aprotinin-like Kunitz domain.

XX Aprotinin; Kunitz domain; human neutrophil elastase; HNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
 KW smoke emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US16349.

XX 16-DEC-1994; 94US-0358160.

XX (PROT-) PROTEIN ENG CORP.

XX Guterman SK, Kent RB, Ladhner RC, Ley AC, Markland W;

XX Roberts BL;

XX WPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg.
 PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
 PT other respiratory disorders

XX Example 23; Page 47; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the
 CC elimination of pathogens and the restructuring of connective tissue.
 CC In cases of reduction of the circulating alpha-1-protease inhibitor
 CC (API or alpha antitrypsin), or the inactivation of API by oxidation
 CC (smoke emphysema), extensive destruction of the lung tissue may
 CC result from uncontrolled elastolytic activity of human neutrophil
 CC elastase. Other respiratory disorders such as cystic fibrosis are
 CC thought to be caused by human neutrophil elastase release by
 CC neutrophils. The genetically engineered human derived Kunitz
 CC domains can be used to treat such respiratory disorders. See

XX AA99146-R39211.

XX AA99146-R39211.

XX Sequence 58 AA;

Thu Jan 29 10:02:43 2004

us-09-700-179a-2.rag

Page 9

Query Match	64.8%	Score 221	DB 17	Length 58
Best Local Similarity	69.1%	Pred. No. 2,7e-19		
Matches	38	Conservative	2	Mismatches 15; Indels 0; Gaps 0;
Qy	3	RPDCCCLPADQPCGVRPRSPSYNNDEKCLFLFYGGCGGNANNFITECESTC	57	
Db	1	RPDCCCLPADQPCGVRPRSPSYNNDEKCLFLFYGGCGGNANNFITECESTC	55	

Search completed: January 23, 2004, 10:24:35
Job time : 29.4613 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 31.2711 Seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179A-22

Sequence: 1 MSQSGILLILGLITLWEVL.....CCGNANFKTIERKSTCAA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	97.4	83	13	Q90W98
2	372	81.2	83	13	Q90W99
3	341	74.5	83	13	Q90W01
4	333	72.7	83	13	Q90W00
5	332	70.3	83	13	Q90W96
6	317	69.2	83	13	Q90W97
7	282	63.8	88	13	Q8AY43
8	291	63.5	88	13	Q8AY41
9	279	60.9	88	13	Q8AY42
10	248	54.1	79	13	Q91351
11	214	46.7	90	13	Q8AY45
12	214	46.7	90	13	Q8AY44
13	193	42.1	90	13	Q8AY46
14	187	40.8	142	5	Q8WP12
15	184	40.2	142	5	Q8WP13
16	183	40.0	59	5	Q9TW98

17	183	40.0	85	13	Q9PTA4	Q9pta4 bungarus mu
18	180	39.3	85	13	Q9TW28	Q9tw28 bungarus mu
19	173	37.8	58	5	Q9TW60	Q9tw60 anemonia su
20	172.5	37.7	82	5	Q8WVB4	Q8wvb4 ixodes scap
21	172	37.6	76	5	Q8T7L9	Q8t7l9 bombyx mori
22	169	36.9	267	6	Q8MI34	Q8mi34 ovis aries
23	169	36.9	506	6	Q8MI33	Q8mi33 ovis aries
24	162	35.4	58	5	Q9TW99	Q9tw99 anemonia su
25	160	34.9	235	11	Q8CI80	Q8ci80 mus musculus
26	160	34.9	235	11	Q8BSB7	Q8bsb7 mus musculus
27	158	34.5	287	13	Q9J424	Q9j424 cyprinus ca
28	158	34.5	366	6	Q28874	Q28874 canis famli
29	155.5	34.0	80	5	Q8T3S7	Q8t3s7 areneus ven
30	154	33.6	1487	5	Q8MPV5	Q8mpv5 caenorhabdi
31	154	33.6	1558	5	Q8I710	Q8i710 caenorhabdi
32	154	33.6	2157	5	Q76840	Q76840 caenorhabdi
33	153.5	33.5	230	11	Q8CE99	Q8ce99 rattus norv
34	153	33.4	759	5	Q8IT91	Q8it91 ancylostoma
35	153	33.4	984	5	Q9GQ02	Q9gq02 calliactis
36	153	33.4	984	5	Q9GQ01	Q9gq01 calliactis
37	153	33.4	2225	5	Q45881	Q45881 caenorhabdi
38	152	33.2	169	6	Q9NOX7	Q9nox7 bos taurus
39	152	33.2	249	5	Q16701	Q16701 caenorhabdi
40	151.5	33.1	154	6	Q9NOX3	Q9nox3 ovis aries
41	151	33.0	277	13	Q8AYE1	Q8aye1 brachydanio
42	150	32.8	113	5	Q9V508	Q9v508 drosophila
43	150	32.8	167	4	Q8NE89	Q8ne89 homo sapien
44	150	32.8	224	4	Q8NAK6	Q8nak6 homo sapien
45	148	32.3	183	6	Q9NOX5	Q9nox5 bos taurus

ALIGNMENTS

RESULT 1

Q90W98 PRELIMINARY; PRT; 83 AA.

AC Q90W98;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Acanthophinae; Pseudonaja.
 OX NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masai P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasma inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masai P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF402327; AAK95522.1;
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor
 SQ SEQUENCE 83 AA; 8983 MW; 3F28548146BA298 CRC64;

Query Match 97.4%; Score 446; DB 13; Length 83;
 Best Local Similarity 97.6%; Pred. No. 8e-46;
 Matches 81; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	Db
1	1
MSGGGLLLGLLTLMVLTLPVSSKDHPRFCCLPAEFGSCKGNVPRTYYADHQCIAET	MSGGGLLLGLLTLMVLTLPVSSKDHPRFCCLPAEFGSCKGNVPRTYYADHQCIAET
60	60
61	1
YGGCGGANNPFTIIECKSTCA	MSGGGLLLGLLTLMVLTLPVSSKDHPRFCCLPAEFGSCKGNVPRTYYADHQCIAET
83	60
61	1
YGGCGGANNPFTIIECKSTCA	MSGGGLLLGLLTLMVLTLPVSSKDHPRFCCLPAEFGSCKGNVPRTYYADHQCIAET
83	60

RESULT 2

ID	Q90W99	PRELIMINARY;	PRT;	83 AA.
AC	Q90W99;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Textilinn.			
OS	Pseudonaja textilis textilis.			
OC	Euryarcha, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Maaci P.P., Lavyn M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,			
RT	"Plasmin inhibitors from the Australian brown snake Pseudonaja			
RT	textilis textilis."			
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Filipovich I.V., Sorokina N.I., Maaci P.P., de Jersey J.,			
RA	Whitaker A.N., Gaffney P.J., Lavyn M.F.;			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF402326; AAK95521.1;			
DR	InterPro; IPR002223; Kuntz BPTI.			
DR	Pfam; PF00014; Kuntz BPTI; 1.			
DR	ProDom; PD000222; Kuntz BPTI; 1.			
DR	SMART; SMO0131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
DR	Protease inhibitor; Serine protease inhibitor.			
QW	SEQUENCE 83 AA; 9158 MW; 366EB82487ACFB61 CRC64;			

Query Match	81.2%	Score 372;	DB 13;	Length 83;
Best Local Similarity	79.5%;	Pred. No. 5.9e-37;		
Matches 66;	Conservative 7;	Mismatches 10;	Indels 0;	Gaps 0

```

Qy      MSSGGLLLLGLLTLMETVLPVSSKDDPKPEELPAEFGSSCKGANVPRFYNAADHHQCLKFI 6
Db      1  MSSGGLLLLGLLTLMETVLPVSSKDDPNPCKLPAETGRCAKAPIPRFYINPROHCIEPL 6
Qy      61  YGCGCGNANNPKTIEBGSKTCAA 83
Db      61  YGCGCGNANNPKTIEBGSKTCAA 83

RESULT 3
Q90WA1  PRELIMINARY;      PRT;      83 AA.
AC      Q90WA1;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Textiliina.
OS      Pseudonaja textilis textilis.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Elapidae; Acanthophinae; Pseudonaja.
OX      NCB1_TaxID=169397;
RN      [1]

```

RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland.
RA Maci P.P., Lavina M.F., Gaffney P.J., Sorokina I.N., Pippovich I.V.,
RT "Plasmin inhibitors from the Australian brown snake *Pseudonaja*
RL textilis textilis";
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[2]

RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.
RA Whitaker A.N., Gaffney P.J., Layin M.F.,
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF402334; AAC95519.1; -
DR InterPro; IPRO02223; Kunitz; BPTI.
DR Pfam; PF00014; Kunitz; BPTI. 1.
DR ProDom; PD000222; Kunitz; BPTI. 1.
DR SMART; SMO031; KU. 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9173 MW; 2045EB50657014221 CRC64;

Query Match	74.5%	Score 341;	DB 13;	length 83;
Best Local Similarity	77.1%;	Pred. No. 3.1e-33;		
Matches 64; Conservative	5;	Mismatches 14;	Indels 0;	Gaps 0

[illegible]

4

ID	Q90WA0	PRELIMINARY;	PRT;	83 AA.
AC	Q90WA0			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Textilinh.			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Leiodontauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Elapidae; Acantophiinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			

P SEQUENCE FROM N.A.,
C TISSUE=venom gland;
C Masati P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.: "N-
A "Plasma inhibitors from the Australian brown snake pseudonaja
T "textilis" textilis.",
T Submitted (AUG-2001) to the EMBL/GenBank/DBJ databses.

RC SEQUENCE FROM N.A.
RP TISSUE-Venom gland;
RA Filippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.
RA Whitaker A.N., Gaffney P.J., Layton M.F.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402325; AAKS5520.1; -
DR InterPro; IPR002223; Kunitz_BPT1.
DR Pfam; PFO0014; Kunitz_BPT1.1.
DR Prodom; PD000222; Kunitz_BPT1.1.
DR SMART; SMO0311; KU; 1
DR PROSITE; PS00286; BPT1_KUNITZ_1; 1.
DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
DR Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9179 NW; 678589MD21175930 CRC64;

Query Match	72.7%;	Score 333;	DB 13;	Length 83
Best Local Similarity	74.7%;	Pred. No. 2.8e-32;		

Matches	62; Conservative	6; Mismatches	15; Indels	0; Gaps	0;
Qy	1	MSGGILLLLGLTLTMEVLTPTVSSDHPKCEGLPAETGSCKNVNRFPYNNADHQCWPI	60		
Db	1	MSGGILLLLGLTLTMEVLTPTVSSDHPKCEGLPAETGSCKNVNRFPYNNADHQCWPI	60		
Qy	61	YGGCGGNNNNPXTIEGKSTCA	83		
Db	61	YGGCGGNNNNPXTIEGKSTCA	83		

ID	Q90W96	PRELIMINARY:	PRT:	83 AA.
AC	Q90W96	01-DEC-2001 (TREMBlrel. 19, Created)		
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Textilinn.			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Leiodontia; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxId=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filpovich I.V.,			
RT	"Plasmin inhibitors from the Australian brown snake Pseudonaja			
RT	textilis textilis."			
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,			
RA	Whitaker A.N., Gaffney P.J., Lavin M.F.;			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF402329; AAK95348.1; -			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI.1.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	ProDom; PD000222; Kunitz_BPTI.1.			
DR	SMART; SM00131; KU.1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
DR	Protease inhibitor; Serine protease inhibitor.			
QW	SEQUENCE 83 AA; 9060 MW; A66DE2692864C58E CRC64;			
Query Match	70.3%; Score 322; DB 13; Length 83;			
Best Local Similarity	72.3%; Pred. No. 5.9e-31;			
Matches	60; Conservative 7; Mismatches 16; Indels 0; Gaps 0			
QY	1 MSSGGLLLLLGLTLMVEVLTPVSSKHDPKFCBLPAETSSCKGNVPRFYNNDDHQCLEFI 60			
DB	1 MSSGGLLLLLGLTLMVEVLTPVSSKHDPKFCBLPAETSSCKGNVPRFYNNDDHQCLEFI 60			
QY	61 YGGCGGNANNPKEITBEKSTCA 83			
DB	61 YGGCGGNANNPKEITBEKSTCA 83			

```

OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Maaci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filpovich I.V.,
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filpovich I.V., Sorokina N.I., Maaci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402328; AAK95523.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.1.
DR ProDom; PD00022; Kunitz_BPTI.1.
DR SMART; SM00131; Ku.1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR KW Protease inhibitor, Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9031 MW; 9CA7FE39D09B191 CRC64;

Query Match .69.2%; Score 117; DB 13; Length 83;
Best Local Similarity .72.3%; Pred. No. 2,3e-30;
Matches 60; Conservative 8; Mismatches 15; Indels 0; Gaps 0.

```

Query Match	Best Local	Matches	Similarity	Conservative	Score	DB	Length
69.2%;	72.3%;	60;	60;	8;	15;	0;	83;
Pred. No. 2,36-30;							
MIsmatches							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
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MIsmatches							
Indels							
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MIsmatches							
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MIsmatches							
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MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							
Gaps							
MIsmatches							
Indels							

RESULT 8

OBAY41

PRELIMINARY; PRT; 88 AA.

AC OBAY41; PRELIMINARY; PRT; 88 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Kunitz inhibitor c (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057888; AAL30070.1; -
 FT NON TER 1
 SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;

Query Match 63.5%; Score 291; DB 13; Length 88;
 Best Local Similarity 68.3%; Pred. No. 3.2e-27;
 Matches 56; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

OY 1 MSSGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 60
 DB 6 MSSGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 65
 61 YGCGGNANFKTIEBKSTCA 82
 66 YGCGGNANFKTIEBKSTCA 87

RESULT 9

OBAY42

PRELIMINARY; PRT; 88 AA.

AC OBAY42; PRELIMINARY; PRT; 88 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Kunitz inhibitor b (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057887; AAL30069.1; -
 FT NON TER 1
 SQ SEQUENCE 88 AA; 9391 MW; 71P9F57D36E7A652 CRC64;

Query Match 60.9%; Score 279; DB 13; Length 88;
 Best Local Similarity 65.4%; Pred. No. 8.9e-26;
 Matches 53; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 MSSGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 60
 DB 6 MSSGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 65
 61 YGCGGNANFKTIEBKSTCA 81
 66 YGCGGNANFKTIEBKSTCA 86

RESULT 10

O91351

PRELIMINARY; PRT; 79 AA.

AC O91351; PRELIMINARY; PRT; 79 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Dendrotoxin K (Fragment).
 OS DENDROTOXIN K, DTXK.
 OC Dendroaspis polylepis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93277850; PubMed=8504088;
 RA Smith L.A., Lataye P.J., Latenotiere H.F., Spain T., Dolly J.O.;
 RT "Cloning and functional expression of dendrotoxin K from black mamba,
 a K+ channel blocker."
 RL Biochemistry 32:5692-5697 (1993).
 DR EMBL; S61886; AAB26998.1; -
 FT HSP; P00981; 1DTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PDO00222; Kunitz_BPTI; 1.
 DR SMART; SM00331; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 FT NON TER 1
 SQ SEQUENCE 79 AA; 8851 MW; DCDFB9AFA07D7D46 CRC64;

Query Match 54.1%; Score 248; DB 13; Length 79;
 Best Local Similarity 62.0%; Pred. No. 4.1e-22;
 Matches 49; Conservative 4; Mismatches 24; Indels 2; Gaps 1;

OY 3 SGGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 62
 DB 1 SGGILLILGLITLMEVLTVPSSKDHKPCFLPATGSGCKGNVPRFYNAHOCLEKPI 58
 63 GCGGNANFKTIEBKSTC 81
 59 GCGGNANFKTIEBKSTC 77

RESULT 11

OBAY45

PRELIMINARY; PRT; 90 AA.

AC OBAY45; PRELIMINARY; PRT; 90 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Beta bungarotoxin B2a chain (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057884; AAL30066.1; -
 FT NON TER 1
 SQ SEQUENCE 90 AA; 10122 MW; AD0FE279D68A910 CRC64;

Query Match 46.7%; Score 214; DB 13; Length 90;
 Best Local Similarity 59.5%; Pred. No. 5.6e-18;
 Matches 44; Conservative 8; Mismatches 20; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLTMEVLTTPVSS-KDHPKFCGLPAETGSCGNVPRFYNNADHHQCKF 59
 DB 6 MSSGGLLLGLTLTMAELTTPVSSRKRRPD-CDKPPDPTKCTVVRAPFYKPSARCKVOF 64
 QY 60 IYGGCGGNANPKT 73
 DB 65 RYGGCGNGNHPKS 78

RESULT 12

Q8AY44 PRELIMINARY; PRT; 90 AA.
 AC Q8AY44;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Beta bungaratoxin B2D chain (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Teal I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057885; AAL30067.1; -.
 FT NON-TER
 SQ SEQUENCE 90 AA; 10281 MW; 15754C179BDE190E CRC64;

Query Match 46.7%; Score 214; DB 13; Length 90;
 Best Local Similarity 59.5%; Pred. No. 5.6e-18;
 Matches 44; Conservative 8; Mismatches 20; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLTMEVLTTPVSS-KDHPKFCGLPAETGSCGNVPRFYNNADHHQCKF 59
 DB 6 MSSGGLLLGLTLTMAELTTPVSSRKRRPD-CDKPPDPTKCTVVRAPFYKPSARCKVOF 64
 QY 60 IYGGCGGNANPKT 73
 DB 65 RYGGCGNGNHPKS 78

RESULT 13

Q8AY46 PRELIMINARY; PRT; 90 AA.
 AC Q8AY46;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Beta bungaratoxin B1 chain (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Teal I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057883; AAL30065.1; -.
 FT NON-TER
 SQ SEQUENCE 90 AA; 10048 MW; E05C2A0D28179726 CRC64;

Query Match 42.1%; Score 193; DB 13; Length 90;
 Best Local Similarity 56.8%; Pred. No. 1.8e-15;
 Matches 42; Conservative 8; Mismatches 22; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLTMEVLTTPVSSKDHPKFCGLPAETGSCGNVPRFYNNADHHQCKF 59

DB 6 MSSGGLLLGLTLTCAELTTPVSSRKRRHDCBPPDKGNC-GSVRAAFYDTRLTKCKAF 64
 QY 60 IYGGCGGNANPKT 73
 DB 65 RYGGCGNGNHPKT 78

RESULT 14

Q8WP12 PRELIMINARY; PRT; 142 AA.
 AC Q8WP12;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Boophilin precursor.
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OX NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pereira P.J., Prusa D., Stuerzebecher J., Sures I., Friedrich T.,
 RA Wentele R., Huber R., Bode W., Fuentes-Prior P.;
 RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
 RT characterization, cloning and three-dimensional model of its complex
 RT with thrombin";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pereira P.J.;
 RA Theais (1999), Universidade do Porto, Oporto, Portugal.
 DR EMBL; AJ304447; CAC82583.1; -.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI_2.
 DR PRINTS; PR00759; BASTCPYASE.
 DR PRODOM; PD000222; Kunitz_BPTI; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 KM Protease inhibitor; Serine protease inhibitor; Signal.
 FT SIGNAL
 FT CHAIN
 FT SIGNAL
 SQ SEQUENCE 142 AA; 15538 MW; 8BBF0008BD42010 CRC64;

Query Match 40.8%; Score 187; DB 5; Length 142;
 Best Local Similarity 57.4%; Pred. No. 1.5e-14;
 Matches 31; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPATGSCGNVPRFYNNADHHQCKFYGGCGGNANPKTIEGKSTCA 83
 DB 20 FCELPADGICAKLPFYNNADHHQCKFYGGCGGNANPKTIEGKSTCA 73

RESULT 15

Q8WP13 PRELIMINARY; PRT; 142 AA.
 AC Q8WP13;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Boophilin precursor.
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OX NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pereira P.J., Prusa D., Stuerzebecher J., Sures I., Friedrich T.,
 RA Wentele R., Huber R., Bode W., Fuentes-Prior P.;
 RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
 RT characterization, cloning and three-dimensional model of its complex
 RT with thrombin";

```

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pereira P.J.;
RL Thesis (1999), Universidade do Porto, Oporto, Portugal.
DR EMBL; AJ304446; CAC82582.1; -.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR ProDom; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR KX Proctase inhibitor; Serine proctase inhibitor; Signal.
FT SIGNAL. 1 15
FT CHAIN 16 142 BOOPHTLIN, ISOFORM G2.
SQ SEQUENCE 142 AA; 1555 MW; EA6EC742D3599705 CRC64;

Query Match
Best Local Similarity 40.2%; Score 184; DB 5; length 142;
Matches 30; Conservative 55.6%; Pred. No. 3.5e-14;
Matches 30; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 30 PCGLPAETGSCGNVPRFYNDHQCLEFYGGCGGANNPRTIEGKSTCA 83
Db 20 PCRLPADGICKALIPRFYNTETGKCTMFSGGCGGNNNPETIEDCKACGA 73

```

Search completed: January 23, 2004, 10:27:16
 Job time : 31.2711 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 7.59859 Seconds

(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179a-22

Sequence: 1 MESSGALLLLGLLTWEVL.....CGGNANFKTIEEGSTCAA 83

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	48.9	61	1	PO0991 vipera ammo
2	212	46.3	57	1	P20229 naja naja (
3	212	46.3	65	1	P25660 bungarus fa
4	209	45.6	57	1	PO0986 naja naja
5	207	45.2	57	1	PO0985 hemachatus
6	207	45.2	65	1	PO0992 vipera ammo
7	201	43.9	85	1	PO0989 bungarus mu
8	192	41.9	58	1	P24541 eristocophi
9	189	41.3	62	1	PO0990 dabola ruse
10	186	40.6	60	1	P10280 anemania su
11	184	40.2	62	1	PO0987 bungarus mu
12	184	40.2	85	1	PO0982 vipera ammo
13	178	38.9	57	1	PO0981 eristocophi
14	178	38.9	57	1	PO0982 vipera ammo
15	172	37.6	55	1	P00984 dendroaspis
16	172	37.6	59	1	P00984 dendroaspis
17	169	36.9	304	1	P00984 dendroaspis
18	167	36.5	58	1	P00984 dendroaspis
19	167	36.5	300	1	P00984 dendroaspis
20	166	36.2	55	1	P00984 dendroaspis
21	166	36.2	302	1	P00984 dendroaspis
22	165	36.0	55	1	P00984 dendroaspis
23	165	36.0	110	1	P00984 dendroaspis
24	164	35.8	58	1	P00984 dendroaspis
25	162	35.4	304	1	P00984 dendroaspis
26	160	34.9	306	1	P00984 dendroaspis
27	159.5	34.8	230	1	P00984 dendroaspis
28	157	34.3	57	1	P00984 dendroaspis
29	155	33.8	58	1	P00984 dendroaspis
30	155	33.8	252	1	P00984 dendroaspis
31	153.5	33.4	100	1	P00984 dendroaspis
32	153	33.4	59	1	P00984 dendroaspis
33	150	32.8	60	1	P00984 dendroaspis

34	150	32.8	235	1	TFP2_HUMAN	P46307 homo sapien
35	148.5	32.4	122	1	UPTI_PIG	Q29100 sus scrofa
36	147.5	32.2	100	1	BPT2_BOVIN	P04815 bos taurus
37	147	32.1	69	1	CRPT_BOVIN	P81162 boophilus m
38	146.5	32.0	102	1	ELAC_TRIYU	Q29143 trichosurus
39	144.5	31.6	197	1	MCPI_MEICP	P82968 melitaea c
40	143	31.2	507	1	SPTI_MOUSE	Q97097 mus musculu
41	141	30.8	60	1	IBPS_BOVIN	P00975 bos taurus
42	141	30.8	60	1	TXCA_DENAN	P81658 dendroaspis
43	141	30.8	763	1	APP2_HUMAN	Q06481 homo sapien
44	140	30.6	57	1	IVB2_DENPO	P00983 dendroaspis
45	140	30.6	351	1	TKD1_BOVIN	Q28201 bos taurus

ALIGNMENTS

RESULT 1	IVB1_VIPAA	STANDARD;	PRT;	61 AA.
ID	IVB1_VIPAA	STANDARD;	PRT;	61 AA.
AC	PO0991;			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom basic protease inhibitor I (Venom trypsin inhibitor I).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Leptidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Viperidae; Viperinae; Vipera.			
OX	NCBI_Taxid=8705;			
RN	[1]			
RC	SEQUENCE.			
RP	TISSUE=Venom;			
RX	MEDLINE=84053385; PubMed=6639951;			
RA	Ritonga A., Meloun B., Gubensek F.;			
RT	"The primary structure of Vipera ammodytes venom trypsin inhibitor			
RL	I."			
CC	Biochim. Biophys. Acta 748:429-435(1983).			
CC	- FUNCTION: This protein inhibits trypsin and kallikrein.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01222; TIVITL.			
DR	HSSP; P31713; ISHP.			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam: PF00014; Kunitz_BPTI; 1.			
DR	ProDom: PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Serine protease inhibitor; Pyrrolidone carboxylic acid.			
FT	MOD_RES 1 1			
FT	DISULFID 7 57			
FT	DISULFID 16 40			
FT	DISULFID 32 53			
SQ	SEQUENCE 61 AA; 6865 MW; FC8285F579FE3795 CRC64;			
Query Match	48.9%; Score 224; DB 1; Length 61;			
Best Local Similarity	62.7%; Pred. No. 3.9e-18;			
Matches	37; Conservative 10; Mismatches 12; Indels 0; Gaps 0;			
Qy	25 KDHKPCFELPAFGSGKGVPRFYVNDHHQCLKFTYGGCGGNANFKTIEEGSTCAA 83			
Db	1 QDHKPCFELPAFGSGKGVPRFYVNDHHQCLKFTYGGCGGNANFKTIEEGSTCAA 59			
RESULT 2	IVB1_NAJNA	STANDARD;	PRT;	57 AA.
AC	P20229;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom trypsin inhibitor.			

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OS Naja naja (Indian cobra).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=35670;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=9109304; PubMed=1702708;
RA Shafer J., Beg O.U., Yin S.-J., Zaidi Z.H., Joernvall H.;
RT Primary structure and functional properties of cobra (Naja naja
RT naja) venom Kunitz-type trypsin inhibitor.";
RL Eur. J. Biochem. 194;337-341(1990).
CC -1- FUNCTION: This protein inhibits trypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S13846; S13846.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6371 MW; AABPD7294ADC12A CRC64;

Query Match 46.3%; Score 212; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 7.6e-17;
Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 28 PKFCELPATGSCCKGNVPRFYNNADHHQCLFITYGGCGGNANPFKTIIEGKSTC 81
Db 2 PKFCELPATGELCKARIRSFHYNRAAQCLFITYGGCGGNANPFKTIIEGKSTC 55

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RESULT 3
ID IVB1_BUNFA STANDARD; PRT; 65 AA.
AC P25660;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitors IX and VIIIB.
OS Bungarus fasciatus (Banded krait).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8613;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=83160048; PubMed=6832893;
RA Liu C.-S., Wu T.-C., Lo T.-B.;
RT "Complete amino acid sequences of two protease inhibitors in the
RT venom of Bungarus fasciatus.";
RL Int. J. Pept. Protein Res. 21;209-215(1983).
CC -1- FUNCTION: Inhibitor of chymotrypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P00980; IDTX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

```

```

KM Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).
SQ SEQUENCE 65 AA; 7294 MW; BA340749E194DB51 CRC64;

Query Match 46.3%; Score 212; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 8.6e-17;
Matches 37; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 25 KDHPKCELPATGSCCKGNVPRFYNNADHHQCLFITYGGCGGNANPFKTIIEGKSTCA 83
Db 1 KNRTFENLLPETERCNALLIPAFYNNHLLKQCXYENYGGCGGNANPFKTIIEGKSTCA 59

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RESULT 4
ID IVB2_NAJNI STANDARD; PRT; 57 AA.
AC P00985;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja naja (Cape cobra).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=8655;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76237547; PubMed=950337;
RA Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
RT "Snake venom proteinase inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
RT (Rhinophis corbra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them.";
RL J. Biochem. 79;559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
CC that of bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01217; TINJVC.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A0287D1 CRC64;

Query Match 45.6%; Score 209; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 1.6e-16;
Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 28 PKFCELPATGSCCKGNVPRFYNNADHHQCLFITYGGCGGNANPFKTIIEGKSTC 81
Db 2 PKFCELPATGELCKARIRSFHYNRAAQCLFITYGGCGGNANPFKTIIEGKSTC 55

RESULT 5
ID IVB2_HEMHA STANDARD; PRT; 57 AA.
AC P00985;
DT 21-JUL-1986 (Rel. 01, Created)

```

DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Ringhale) (Sapedon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Hemachatus.
 NCBI_TaxID=8626;
 [1]
 RP SEQUENCE.
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokana Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 polybasic peptide inhibitors from the venoms of Hemachatus haemachatus
 (Ringhale's cobra) and Naja naja (Cape cobra) and the complete amino
 acid sequences of two of them."
 RL J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC -1- bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC PIR: A01216; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS02279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7F2A CRC64;
 QY Query Match 45.2%; Score 207; DB 1; Length 57;
 Best Local Similarity 66.7%; Pred. No. 2, 7e-16;
 Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
 DB 28 PRCCELPARTGSCGNVPRPYNADHHQCKPFIYGGCGGNANFKTIEGKSTCA 81
 2 PRCCELPARTGSCGNVPRPYNADHHQCKPFIYGGCGGNANFKTIEGKSTCA 55
 RESULT 6
 ID IYB3_VIPAA STANDARD; PRT; 65 AA.
 AC P00952;
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
 OS Vipera ammodytes ammodytes (Western sand viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 NCBI_TaxID=8705;
 [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Ritonja A., Meloun B., Gubensek F.;
 RT "The primary structure of Vipera ammodytes venom chymotrypsin
 inhibitor."
 RL Biochim. Biophys. Acta 746:138-145(1983).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; A01223; TIVIVC.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS02279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17 18
 SQ SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7C057 CRC64;
 QY Query Match 45.2%; Score 207; DB 1; Length 65;
 Best Local Similarity 61.0%; Pred. No. 3, 1e-16;
 Matches 36; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
 DB 25 KDRPCELPARTGSCGNVPRPYNADHHQCKPFIYGGCGGNANFKTIEGKSTCA 83
 1 KDRPCELPARTGSCGNVPRPYNADHHQCKPFIYGGCGGNANFKTIEGKSTCA 59
 RESULT 7
 ID IYB2_BUNMU STANDARD; PRT; 85 AA.
 AC P00989; O42299; Q9PVB8; Q9PVB3;
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Beta bungarotoxin B2 chain precursor.
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NCBI_TaxID=8616;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=98359733; PubMed=9693106;
 RA Wu P.-F., Wu S.N., Chang C.-C., Chang L.-S.;
 RT "Cloning and functional expression of B chains of beta-bungarotoxins
 from Bungarus multicinctus (Taiwan banded krait)."
 RL Biochem. J. 334:87-92(1998).
 [2]
 RP SEQUENCE OF 1-82 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20363696; PubMed=10903499;
 RA Wu P.-F., Chang L.-S.;
 RT "Genetic structures of A chain and B chain of beta-bungarotoxin from
 Taiwan banded krait (Bungarus multicinctus). A chain genes and B chain
 genes do not share a common origin."
 RL Eur. J. Biochem. 267:4668-4675(2000).
 [3]
 RP SEQUENCE OF 25-85.
 RC TISSUE=Venom;
 RX MEDLINE=82239269; PubMed=7096304;
 RA Kondo K., Toda H., Narita K., Lee C.-Y.;
 RT "Amino acid sequence of beta 2-bungarotoxin from Bungarus
 multicinctus venom. The amino acid substitutions in the B chains."
 RL J. Biochem. 91:1519-1530(1982).
 [4]
 RP SEQUENCE OF 25-63.
 RX MEDLINE=95031955; PubMed=7945237;
 RA Chu C.C., Chu S.T., Chen S.W., Chen Y.H.;
 RT "The non-phospholipase A2 subunit of beta-bungarotoxin plays an
 important role in the phospholipase A2-independent neurotoxic effect:
 characterization of three isoforms with a common phospholipase A2
 subunit."
 RL Biochem. J. 303:171-176(1994).
 [5]
 RP REVIEW.
 RX MEDLINE=20396379; PubMed=10936627;
 RA Rowan E.G.;
 RT "What does beta-bungarotoxin do at the neuromuscular junction?"
 RL Toxicon 39:107-118(2001).
 CC -1- FUNCTION: Beta-2 bungarotoxin is a presynaptic neurotoxin of the

CC venom. The B chain is homologous to venom basic protease
 CC inhibitors but has no protease inhibitor activity and is non-
 CC toxic.
 CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
 CC The A chains have phospholipase A2 activity and the B chains show
 CC homology with the basic protease inhibitors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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CC -----
 CC EMBL: Y12101; CAA72810.1; -
 CC EMBL: AJ251224; CAB62504.1; -
 CC PDB: 1BUN; 03-APR-96.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF00014; Kunitz_BPTI_1.
 CC ProDom: PD000222; Kunitz_BPTI_1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC Toxin: Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
 CC KMW: Toxin; Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
 CC FT: SIGNAL 1 24
 CC FT: CHAIN 1 85
 CC FT: DOMAIN 31 81
 CC FT: DISULFID 31 81
 CC FT: DISULFID 40 64
 CC FT: DISULFID 56 77
 CC FT: DISULFID 79 79
 CC FT: ACT_SITE 41 42
 CC FT: CONFLICT 44 44
 CC FT: CONFLICT 65 70
 CC FT: CONFLICT 82 83
 CC FT: SEQUENCE 85 AA; 9568 MW; FE95A59AF92BF2MA CRC64;
 CC
 CC Query Match 43.9%; Score 201; DB 1; Length 85;
 CC Best Local Similarity 58.1%; Pred. No. 1.8e-15;
 CC Matches 43; Conservative 8; Mismatches 21; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLMEVLTVPSS-KDHPKFCLEPAETGSCGNVPRRYNADHHQICLF 59
 DB 1 MSSGGLLLGLTLCAELTVPSSSRKRPD-CDKPPDTKICQTVVRAFYKPSARCVQF 59
 QY 60 IYGGCGGNANPKT 73
 DB 60 RYGGCGNGNHPKS 73

RESULT 8
 IVBC_OPHNA STANDARD; PRT; 58 AA.
 AC P82966;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom chymotrypsin inhibitor.
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Elapidae; Elapinae; Ophiophagus.
 CC NCBI_Taxid=8665;
 CC [1]
 CC SEQUENCE.
 CC TISSUE=Venom gland;
 CC MEDLINE=21248396; PubMed=11350064;
 CC Chang L.-S., Chung C., Huang H.-B., Lin S.-R.;
 CC "Purification and characterization of a chymotrypsin inhibitor from

RT the venom of Ophiophagus hannah (King Cobra).";
 RL Biochem. Biophys. Res. Commun. 283:862-867(2001).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC HSSP: P00981; IDTK.
 CC DR GO: GO:0005576; C:extracellular; NAS.
 CC DR GO: GO:0004867; F:serine protease inhibitor activity; IDA.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF00014; Kunitz_BPTI_1.
 CC PRINTS: PR00759; BASICTPASE.
 CC ProDom: PD000222; Kunitz_BPTI_1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC KMW: Serine protease inhibitor.
 CC FT: DISULFID 6 56
 CC FT: DISULFID 15 39
 CC FT: DISULFID 31 52
 CC FT: ACT_SITE 16 17
 CC FT: SEQUENCE 58 AA; 6499 MW; 3EB44C85F0843D8A CRC64;
 CC
 CC Query Match 41.9%; Score 192; DB 1; Length 58;
 CC Best Local Similarity 63.0%; Pred. No. 1.2e-14;
 CC Matches 34; Conservative 2; Mismatches 18; Indels 0; Gaps 0;

QY 28 PKFCLEPAETGSCGNVPRRYNADHHQICLFYGGCGGNANPKTEBGKSTC 81
 DB 3 PKFCLEPAETGSCGNVPRRYNADHHQICLFYGGCGGNANPKTEBGKSTC 81

RESULT 9
 IVBT_ERIMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis macmahoni (Leaf-nosed viper).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Viperinae; Eristocophis.
 CC NCBI_Taxid=8702;
 CC [1]
 CC SEQUENCE.
 CC TISSUE=Venom;
 CC MEDLINE=92077130; PubMed=1743283;
 CC Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 CC "Purification and characterization of a Kunitz-type trypsin inhibitor
 CC from leaf-nosed viper venom.";
 CC FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC PIR: S19327; S19327.
 CC DR HSSP: P00981; IDTK.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF00014; Kunitz_BPTI_1.
 CC PRINTS: PR00759; BASICTPASE.
 CC ProDom: PD000222; Kunitz_BPTI_1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC KMW: Serine protease inhibitor.
 CC FT: DISULFID 2 52
 CC FT: DISULFID 11 35
 CC FT: DISULFID 27 48
 CC FT: ACT_SITE 12 13
 CC FT: SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;
 CC
 CC Query Match 41.3%; Score 189; DB 1; Length 62;
 CC Best Local Similarity 59.3%; Pred. No. 2.8e-14;

Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 30 FCELPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTCA 83
DB 1 FCTLPDPGCKAHIPRYNPNASKCNFTYGGCGGNANFETRAECRTCA 54

RESULT 10
ID IVB2_DABRU STANDARD; PRT; 60 AA.
AC P00950;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II (RVV-II).
OS Dabola russelli siamensis (Siamese Russell's viper) (Vipera russelli siamensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabola.
NCBI_TaxID=8708;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=75060360; PubMed=4436285;
RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
RT "Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isolated from the venom of Russell's viper (Vipera russelli)."
RT J. Biochem. 76:721-733(1974).
CC -1- FUNCTION: This inhibitor has activity similar to bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P10646; IADZ.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Prodom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT ACT_SITE 17 18
SQ SEQUENCE 60 AA; 6850 MW; 5A7DCB9554CE6A2 CRC64;

Query Match 40.6%; Score 186; DB 1; Length 60;
Best Local Similarity 53.6%; Pred. No. 5.9e-14;
Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 26 DHPKPELPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 81
DB 2 DRPTPCULAPESGCRGHLRIYNNLSNCKKVFYGGCGGNANFETRDCEKSTC 57

RESULT 11
ID IP52_ANESU STANDARD; PRT; 62 AA.
AC P10280;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor 5 II (SA5 II).
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nymphaeae; Actiniidae; Anemonia.
NCBI_TaxID=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone

RT Anemonia sulcata.";
RL Mech. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide from the sea anemone Metridium senile."
RL Naturwissenschaften 74:395-396(1987).
CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S07451; S07451.
DR HSSP; P31713; ISHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55
FT DISULFID 14 38
FT DISULFID 30 51
FT ACT_SITE 15 16
FT VARIANT 13 13
FT VARIANT 16 16
FT VARIANT 17 17
FT VARIANT 25 25
FT VARIANT 28 28
FT VARIANT 39 39
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 40.2%; Score 184; DB 1; Length 62;
Best Local Similarity 58.8%; Pred. No. 1e-13;
Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 31 CELPAPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 81
DB 5 CELPKVGPGRARPRFYNNSSKRCCKFYGGCGGNANFHTIECKKVC 55

RESULT 12
ID IVB1_BUNMU STANDARD; PRT; 85 AA.
AC P00987; O42298; P00988;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta bungarotoxin B1 chain, major component precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
NCBI_TaxID=6616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=98359733; PubMed=9693106;
RA Wu P.-F., Wu S.-N., Chang C.-C., Chang L.-S.;
RT "Cloning and functional expression of B chains of beta-bungarotoxins from Bungarus multicinctus (Taiwan banded krait)."
RT Biochem. J. 334:87-92(1998).
RN [2]
RP SEQUENCE OF 25-85.
RC TISSUE=Venom;
RX MEDLINE=78109400; PubMed=624701;
RA Kondo K., Narita K., Ise C.-Y.;
RT "Amino acid sequences of the two polypeptide chains in beta-bungarotoxin from the venom of Bungarus multicinctus.";
RT J. Biochem. 83:101-115(1978).
RN [3]
RP MUTAGENESIS OF CYS-32.
RX MEDLINE=21589307; PubMed=11732693;

DE Venom basic protease inhibitor K (Dendrotoxin delta-DatX) (Toxin
DS SSI1G3)
OS Dendroaspis angusticeps (Eastern green mamba).
OC Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossae; Serpentes; Colubroidae;
OX Elapidae; Elapinae; Dendroaspis.
NCBI_TaxID=8618;
RN [1]
RP SEQUENCE.
RX MEDLINE=81045446; PubMed=7429422;
RA Joubert F.J., Taljaard N.;
RT "Snake venoms. The amino acid sequences of two proteinase inhibitor
homologues from dendroaspis angusticeps venom.";
RN Hoppe-Seyler's Z. Physiol. Chem. 361:661-674.(1980).
[2]
RP SEQUENCE.
RX MEDLINE=88318591; PubMed=2457792;
RA Bernstein C.G., Sorensen R.G., Brown W.E., Krueger B.K.,
Blaustein M.P.;
RT "Four polypeptide components of green mamba venom selectively block
certain potassium channels in rat brain synaptosomes.";
RL Mol. Pharmacol. 34:152-159(1988).
CC -1- FUNCTION: This protease inhibitor homolog has very low toxicity.
CC It blocks voltage-gated potassium channels and facilitate
neurotransmitter release.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: LD(50) is 15 mg/kg by intravenous injection.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A91691; TIEPVA.
DR HSSP; P00981, IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF000014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00331; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Toxin; Neurotoxin;
KM Potassium channel inhibitor.
KW DISULFID 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT FT 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BIND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6574 MW; A4070CBBB141DE93 CRC64;

Query Match 38.9%; Score 178; DB 1; Length 57;
Best Local Similarity 58.5%; Pred. No. 4.3e-13;
Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0.

OY 29 KPCELPVETSGCKGNVRFPYYNDHQCLEPIYGGCGNNNPFITEGSKTC 81
DB 3 KYCKLPRYPGPCKKXIIPSYFKWKAKQCLPDVSGCGMNRPFITISCRATC 55

RESULT 14
ID VIBK_DENPO STANDARD; PRT; 57 AA.
AC P00981;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Venom basic protease inhibitor K (Dendrotoxin K).
OS Dendroaspis polyleps polyleps (Black mamba).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossae; Serpentes; Colubroidae;
OX Elapidae; Elapinae; Dendroaspis.
NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=77158069; PubMed=857902;
RA Strzydom D.J.;
RT "Snake venom toxins. The amino acid sequence of toxin Vi2, a
homologue of pancreatic trypsin inhibitor, from dendroaspis polyleps

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RT poly(lep) (black mamba) venom."
RL Biochim. Biophys. Acta 491:361-369(1977).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=94076347; PubMed=8254670;
RA Bernik K.D.; Guentert P.; Wuehrlich K.;
RT "Nuclear magnetic resonance solution structure of dendrotoxin K from
   the venom of Dendroaspis polylepsis polylepsis."
RL J. Mol. Biol. 234:735-750(1993).
CC -1- FUNCTION: This protein is much less toxic to mice than is whole
   venom. It inhibits trypsin slightly, but chymotrypsin not at all.
   It is a highly selective blocker of voltage-gated potassium
   channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: LD(50) IS 30 MG/KG BY INTRAVENOUS INJECTION.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PDB, 1DK; 31-JAN-94.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; toxin; Neurotoxin; Ionic channel inhibitor;
   3D-structure; Potassium channel inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT HELIX 3 6
FT STRAND 18 24
FT TURN 25 28
FT STRAND 29 35
FT STRAND 45 45
FT HELIX 48 55
SQ SEQUENCE 57 AA; 6566 MW; C30818PFB3C41CB87 CRC64;

Query Match 38.9%; Score 178; DB 1; Length 57;
Best Local Similarity 58.5%; Pred. No. 4,3e-13;
Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 29 KFCLEPAETGSGKGVPRFYTNADHQCLEKRYGCGGANNANFKTIEGKSTC 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 KYCKLPLRIGPCRKIPSPFYKWKAKQCLPFDYSGCGGANNANFKTIEGKSTC 55

RESULT 15
CSTI_BOMMO
ID CSTI_BOMMO STANDARD; PRT; 55 AA.
AC P81902;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;
   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
   Bombycidae; Bombyx.
OX NCB1_TaxID=7091;
RX SEQUENCE AND CHARACTERIZATION.
RP STRAIN=Asahi;
RX MEDLINE=99115431; PubMed=9914483;
RA Kurioka A.; Yamazaki M.; Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
   Bombyx mori."
RL Eur. J. Biochem. 259:120-126(1999).
CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
   activity by forming a low-dissociation complex with trypsin. May
   play an important part in regulating proteolytic activity in the
   silk gland or protecting silk proteins from degradation during
   histolysis.
CC -1- SUBUNIT: Monomer.

```

```

CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
   gland.
CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
   middle silk glands during the final stage of larval growth with
   highest expression before the onset of spinning.
CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR HSSP; P31713; ISHP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Developmental protein; Serine protease inhibitor.
FT DISULFID 4 54 BY SIMILARITY.
FT DISULFID 13 37 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY
   SIMILARITY).
SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2B8E59 CRC64;

Query Match 37.6%; Score 172; DB 1; Length 55;
Best Local Similarity 54.9%; Pred. No. 1.9e-12;
Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 31 CELPAPETGSGKGVPRFYTNADHQCLEKRYGCGGANNANFKTIEGKSTC 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 CLPIKTPCKGSPPRAYDSSBDCVCFIYGGGANNANFKTIEGKSTC 54

Search completed: January 23, 2004, 10:25:15
Job time : 7.59859 secs

```

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 12.8592 Seconds
(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179a-22

Sequence: 1 MSGGILLILGLTLMWEVL.....CGGNANFKTIEBKSTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	54.1	79	1	TIEPVK K+ channel blocker
2	224	48.9	61	1	TIVTIL venom basic protei
3	212	46.3	57	2	S13846 venom animal Kunitt
4	209	45.6	57	1	TINIVC venom basic protei
5	207	45.2	57	1	TIRIVZ venom basic protei
6	207	45.2	65	1	TIVIVC venom basic protei
7	202	44.1	62	2	A44180 calcatoxin serine
8	189	41.3	62	2	S19327 venom basic protei
9	186	40.6	60	1	TIVRZ2 venom basic protei
10	184	40.2	62	2	S07451 proteinase inhibit
11	178	38.9	57	2	TIBPVA venom basic protei
12	174	38.0	57	2	A59204 basic proteinase i
13	172	37.6	57	2	B59399 short epsilon-dend
14	172	37.6	59	1	TIBPED venom basic protei
15	172	37.6	59	2	A59399 long epsilon-dendr
16	169	36.9	304	1	JC2264 tissue factor path
17	167.5	36.6	299	2	I46937 tissue factor path
18	167	36.5	300	2	S12143 lipoprotein-aseect
19	166	36.2	55	2	S30332 proteinase inhibit
20	166	36.2	110	1	TIRTKR tissue factor path
21	165	36.0	110	1	TITTOR basic proteinase i
22	164	35.8	58	1	TITHAK isoinhibitor K (BP
23	162	35.4	304	1	TITHUK tissue factor path
24	158	34.5	396	2	S53325 tissue factor path
25	157	34.3	57	2	S12957 venom animal Kunitt
26	154	33.6	1558	2	C89114 protein C37C3.6a
27	154	33.6	2167	2	T34335 hypothetical prote
28	153.5	33.5	100	1	TIBO basic proteinase i
29	153	33.4	59	1	VIEPIA venom basic protei

30	153	33.4	2225	2	T26063 hypothetical prote
31	152	33.2	249	2	T32060 hypothetical prote
32	150	32.8	60	1	TIEPVI venom basic protei
33	150	32.8	235	2	A54951 tissue factor path
34	148.5	32.4	132	1	A55115 uterine plasmin/tr
35	147.5	32.2	100	1	TIBOSP spleen basic prote
36	146.5	32.0	102	1	S69288 early lactation pr
37	144	31.4	111	2	S41082 amyloid precursor
38	144	31.4	805	2	T34212 hypothetical prote
39	143	31.2	59	2	S00371 isoprotein G1 -
40	143	31.2	747	2	JH0773 Alzheimer's diseas
41	142	31.0	1965	2	T33216 hypothetical prote
42	141	30.8	58	2	S10063 isoprotein G2 -
43	141	30.8	60	1	TIBOR serum basic protei
44	141	30.8	60	2	A36989 calcitriol - eas
45	141	30.8	751	2	A49974 beta-amyloid precu

ALIGNMENTS

RESULT 1

K+ channel blocker dendrotoxin K - black mamba
C/Species: Dendroaspis polylepsis polylepsis (black mamba)
C/Date: 30-Nov-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C/Accession: A49291; A01213
R/Smith, L.A.; Lafaye, P.J.; Lapenotiere, H.F.; Spain, T.; Dolly, J.O.
Biochemistry 32, 5692-5697, 1993
A/Title: Cloning and functional expression of dendrotoxin K from black mamba, a K+ char
A/Reference number: A49291; PMID:93277850; PMID:8504088
A/Accession: A49291
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-79 <SM>
A/Cross-references: GB:561886; NID:G385317; PID:AA826998.1; PID:G385318
A/Note: sequence extracted from NCBI backbone (NCBI:133053, NCBI:P:133054)
A/Note: the source is designated as Dendroaspis polylepsis
R/Strydom, D.J.
Biochim. Biophys. Acta 491, 361-369, 1997
A/Title: Snake venom toxins. The amino acid sequence of toxin Vi2, a homologue of panc
A/Reference number: A90617; PMID:77158069; PMID:857902
A/Accession: A01213
A/Molecule type: protein
A/Residues: 23-79 <STR>
C/Comment: This protein is much less toxic to mice than is whole venom. It inhibits try
C/Suprafamily: basic proteinase inhibitor; animal Kunittz-type proteinase inhibitor homc
C/Keywords: serine proteinase inhibitor; venom
F:27-77/Domain: animal Kunittz-type proteinase inhibitor homology <BPI>
F:27-77,36-60,52-73/Disulfide bonds: #status predicted

Query Match 54.1%; Score 248; DB 1; Length 79;
Best Local Similarity 62.0%; Pred. No. 1.4e-20;
Matches 49; Conservative 4; Mismatches 24; Indels 2; Gaps 1;

Qy 3 SCGLILGLTLMWEVLTPVSSKHPRCELPATGSCGVNPPRYNADHQCIFYG 62
Db 1 SGILLILGLTLMWEVLTPVSGA-AKYCKPLRIGPCKKIPSTYRKAKKQCLPDIS 58
Oy 63 GCGGNANFKTIEBKSTC 81
Db 59 GCGGNANFKTIEBKSTC 77

RESULT 2

TIVTIL venom basic proteinase inhibitor I - western sand viper
N/Alternate names: venom trypsin inhibitor I
C/Species: Viper a ammodytes ammodytes (western sand viper)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
C/Accession: A01222
R/Ritconja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 748, 429-435, 1983

C.Species: *Oxyuranus scutellatus scutellatus* (Australian taipan)
C.Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C.Accession: A44180
R.Possani, L.D.; Martin, B.M.; Yatani, A.; Mochica-Morales, J.; Zamudio, F.Z.; Guirrola, R.; Toxicon 30, 1333-1364, 1992
A.Title: Isolation and physicochemical characterization of taipatoxin, a complex toxin w
R.Reference number: A44180, MIMD:93134601, PMID:1485334

A:Accession: A44180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Experimental source: subsp. scutellatus, venom
A:Note: sequence extracted from NCBI backbone (NCBIP:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 44.1%; Score 202; DB 2; Length 62;
Best Local Similarity 61.4%; Pred. No. 1,4e-15;
Matches 35; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 25 KDHPKCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 81
Db 1 KDHPKCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57

RESULT 8

venom basic proteinase inhibitor - leaf-nosed viper
N:Alternate names: trypsin inhibitor (Kunitz-type)
C:Species: Eristocophis macdonaldi (leaf-nosed viper)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C:Accession: S19327
R:Submitted: A.R.; Zaidi, Z.H.; Joernvall, H.
PDBS Lett. 294, 141-143, 1991
A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from leaf-
A:Reference number: S19327; PMID:92077130; PMID:1743283
A:Accession: S19327
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <STD>

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 41.3%; Score 189; DB 2; Length 62;
Best Local Similarity 59.3%; Pred. No. 4e-14;
Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 30 FCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTCA 83
Db 1 FCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTCA 54

RESULT 9

venom basic proteinase inhibitor II - Russell's viper
C:Species: Vipera russelli (Russell's viper)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01221
R:Takahashi, H.; Iwanga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.
J. Biochem. 76, 721-733, 1974
A:Title: Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isolat
A:Reference number: A01221; PMID:75060360; PMID:4436285
A:Accession: A01221
A:Molecule type: protein
A:Residues: 1-60 <TK>

C:Comment: This inhibitor has activity similar to that of bovine basic protease inhibiti
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 40.6%; Score 186; DB 1; Length 60;
Best Local Similarity 53.6%; Pred. No. 8,4e-14;
Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 26 DHPKCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 81
Db 2 DHPKCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57

RESULT 10

proteinase inhibitor 5.II - snake-locks sea anemone
C:Species: Anemonia sulcata (snake-locks sea anemone)
C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: S07451; B27222
R:Wunderer, G.; Machleidt, W.; Fritzt, H.
Meth. Enzymol. 80, 816-820, 1981

A:Title: The broad-specificity proteinase inhibitor 5.II from the sea anemone Anemonia
A:Reference number: S07451
A:Accession: S07451
A:Molecule type: protein
A:Residues: 1-59 <MTN>

A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R:Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der
A:Reference number: A94700
A:Accession: B27222

A:Molecule type: protein
A:Residues: 1-38, 'R', '40', 'B', '42', 'BE', '45-48', 'ZZ', '51', 'Z', '53-62 <KRE>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 40.2%; Score 184; DB 2; Length 62;
Best Local Similarity 58.8%; Pred. No. 1,4e-13;
Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 31 CELPAPVAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 81
Db 5 CELPAPVAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 55

RESULT 11

venom basic proteinase inhibitor K - eastern green mamba
N:Alternate names: dendrotoxin delta-Darx
C:Species: Dendroaspis angusticeps (eastern green mamba)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C:Accession: A91691; C32508; A01213
R:Joubert, P.J.; Taljaard, N.
Hoppe-seyler's Z. Physiol. Chem. 361, 661-674, 1980
A:Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroasp
A:Reference number: A91691; PMID:81045446; PMID:7429422
A:Accession: A91691
A:Molecule type: protein
A:Residues: 1-57 <JOU>

R:Benjamin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
Mol. Pharmacol. 34, 152-159, 1988
A:Title: Four polypeptide components of green mamba venom selectively block certain pot.
A:Reference number: A93137; PMID:88318591; PMID:2457792
A:Accession: C32508
A:Molecule type: protein
A:Residues: 1-21 <BEN>

A:Note: the amino acid composition of the inhibitor is identical with that predicted fr
C:Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C:Keywords: venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 38.9%; Score 178; DB 1; Length 57;
Best Local Similarity 58.5%; Pred. No. 6,2e-13;
Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 29 KCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 81
Db 3 KCELPALPAGTSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 55

RESULT 12

A59204
basic proteinase inhibitor - great pond snail
N/Alternate names: trypsin inhibitor
C/Species: Lymnaea stagnalis (great pond snail)
C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 17-Mar-2000
C/Accession: A59204
R/Tagline: G
submitted to the Protein Sequence Database, March 2000
A/Description: Lymnaea trypsin inhibitor.
A/Reference number: A59204
A/Accession: A59204
A/Molecule type: protein
A/Residues: 1-57 <NA>
A/Experimental source: albumen gland
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: glycoprotein; serine proteinase inhibitor
F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/5-55/Disulfide bonds: #status predicted
F/15/Inhibitory site: lys (trypsin) #status predicted
F/24/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 38.0%; Score 174; DB 2; Length 57;
Best Local Similarity 54.9%; Pred. No. 1.7e-12;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 31 CELPAETGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTIKTEGKSTC 81

DB 5 CSIPSEFGPCCKGNFLRYHNSSTNACDFVGGCGGANNPDDIDCKKAC 55

RESULT 13

B59399
short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps
C/Species: Dendroaspis angusticeps
C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002
C/Accession: B59399
R/Signle: R.; Hackert, M.; Aird, S.D.
Toxicon 40; 297-308, 2002
A/Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis
A/Reference number: A59399
A/Accession: B59399
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-57 <AIR>
A/Note: trypsin inhibitor; K+ channel antagonist
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F/5-55/Disulfide bonds: #status experimental
F/14-36/Disulfide bonds: #status experimental
F/30-51/Disulfide bonds: #status experimental

Query Match 37.6%; Score 172; DB 2; Length 57;
Best Local Similarity 54.5%; Pred. No. 2.9e-12;
Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKFCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTIKTEGKSTC 81

DB 1 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 55

RESULT 14

TIRPBD
venom basic proteinase inhibitor B - black mamba
C/Species: Dendroaspis polyolepis polyolepis (black mamba)
C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C/Accession: A01215
R/Joubert, P.J.; Stridom, D.J.
Eur. J. Biochem. 87; 191-198, 1978
A/Title: Snake venoms: the amino-acid sequence of trypsin inhibitor B of Dendroaspis pol
A/Reference number: A01215; MUID:78214615; PMID:66868
A/Accession: A01215
A/Molecule type: protein
A/Residues: 1-59 <JOU>

A/Note: this protein inhibits trypsin and binds transition metal ions such as copper at
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom
F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/7-57/Disulfide bonds: #status predicted

Query Match 37.6%; Score 172; DB 1; Length 59;
Best Local Similarity 54.5%; Pred. No. 3e-12;
Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKFCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTIKTEGKSTC 81

DB 3 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 57

RESULT 15

A59399
long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps
C/Species: Dendroaspis angusticeps
C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002
C/Accession: A59399
R/Signle: R.; Hackert, M.; Aird, S.D.
Toxicon 40; 297-308, 2002
A/Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis
A/Reference number: A59399
A/Accession: A59399
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-59 <AIR>
A/Note: trypsin inhibitor; K+ channel antagonist
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F/7-57/Disulfide bonds: #status experimental
F/15-40/Disulfide bonds: #status experimental
F/32-53/Disulfide bonds: #status experimental

Query Match 37.6%; Score 172; DB 2; Length 59;
Best Local Similarity 54.5%; Pred. No. 3e-12;
Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKFCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTIKTEGKSTC 81

DB 3 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 57

Search completed: January 23, 2004, 10:26:11
Job time : 12.8592 secs

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 40.0387 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179A-22

Perfect score: 458

Sequence: 1 MSGGILLGLLTLMELT.....CGGNANKTIECKSTCA 83

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	458	100.0	83	AAV15148
2	372	81.2	83	AAV15147
3	342	74.7	59	AAV15141
4	341	74.5	83	AAV15145
5	333	72.7	83	AAV15146
6	317	69.2	83	AAV15149
7	308	67.2	83	AAV15150
8	256	55.9	59	AAV15140
9	239	52.2	60	AAV15151

10	225	49.1	59	AAV15138
11	218	47.6	60	AAV15153
12	217	47.4	59	AAV15139
13	211	46.1	58	AAV15146
14	201	43.9	59	AAV15142
15	193	42.1	60	AAV15154
16	192	41.9	59	AAV15143
17	178	38.9	57	AAV15153
18	172	37.6	58	AAV15191
19	170	37.1	58	AAV15142
20	169	36.9	304	AAV15139
21	168	36.7	58	AAV15145
22	166	36.2	58	AAV15182
23	166	36.2	58	AAV15197
24	166	36.2	302	AAV15001
25	166	36.2	302	AAV15153
26	165	36.0	58	AAV15195
27	165	36.0	83	AAV15195
28	164	35.8	58	AAV15195
29	164	35.8	111	AAV15195
30	163	35.6	161	AAV15195
31	163	35.6	291	AAV15195
32	163	35.6	291	AAV15195
33	162	35.4	58	AAV15194
34	162	35.4	160	AAV15194
35	162	35.4	183	AAV15146
36	162	35.4	225	AAV15195
37	162	35.4	286	AAV15195
38	162	35.4	261	AAV15171
39	162	35.4	262	AAV15170
40	162	35.4	265	AAV15170
41	162	35.4	276	AAV15170
42	162	35.4	276	AAV15170
43	162	35.4	276	AAV15170
44	162	35.4	276	AAV15170
45	162	35.4	276	AAV15170

ALIGNMENTS

RESULT 1	AAV15148	standard; Protein: 83 AA.
AC	AAV15148;	
XX	07-FEB-2000 (first entry)	
XX	Proform of Txln 4 protein.	
XX	Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;	
XX	Australian brown snake; conserved cysteine residue; stability; control;	
XX	haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;	
XX	fluidity of blood; alleviates; blood loss; major surgery; trauma; enzyme;	
XX	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;	
XX	reduced propensity; chromoblasts.	
XX	Pseudonaja textilis textilis.	
XX	Key	Location/Qualifiers
XX	Peptide	1..24
XX	Protein	/label= Leader peptide
XX		25..83
XX		/note= "Textilin-4"
XX	W0958569-A1.	
XX	18-NOV-1999.	
XX	PD	
XX	07-MAY-1999;	99WO-AU00343.
XX		

Txln 1 Plasmin inh
Plasmin inhibitor
Txln 2 Plasmin inh
Aprotinin-like Kun
Txln 5 Plasmin inh
Plasmin inhibitor
Txln 6 Plasmin inh
Protease-inhibitor
Kallikrein-inhibitor
Human Lact-K2 deri
Lact gene product.
Lact Kunitz domain
Kallikrein inhibit
Genetically engine
Lact. Rattus ratt
Lipoprotein-associ
Genetically engine
Human aprotinin-11
Kunitz-type protea
Synthetic yeast le
TPPI chimeric prot
Human Tifapinix.
Human Tifapinix-A5
Genetically engine
Lact fragment 1 -
Ser-(Glu15-Thr161)
Angiotensin conver
Ser(Asp1-Thr255)-E
Ser(Asp1-Glu245)-E
Ser(Asp1-Ser248)-
Ser(Asp1-Ile253)-
TPPI mucin K36R.
Recombinant non-gl
Human tissue facto
Human tissue facto

```

PR 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASI P P.
PA (LAVI/) LAVIN M P.
PA (GAF/) GAFNEY P J.
PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
DR N-PSDB; AAZ20927.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Claim 40d; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textillinin protein, Txln 4,
CC that is a single stage competitive inhibitor of plasmin. It is isolated
CC from the Australian brown snake, Pseudonaja textilis textilis. It has
CC six conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln has high
CC specificity for plasmin and low inhibitory efficiency, that can
CC transiently affect the delicate balance between enzymes and inhibitors
CC of the fibrinolytic system, controlling the fluidity of blood. The
CC plasmin inhibitors are useful for alleviating blood loss, following
CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC propensity to cause thrombosis.
XX
XX Sequence 83 AA;
SQ
Query Match 100.0%; Score 458; DB 21; Length 83;
Best Local Similarity 100.0%; Pred. No. 4e-48;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSGGILLLLGLLTMEVLTTPVSSKDRHPFCELPAETGSCKGNVPRFYNNADHOCLEKI 60
DB 1 MSSGGILLLLGLLTMEVLTTPVSSKDRHPFCELPAETGSCKGNVPRFYNNADHOCLEKI 60
QY 61 YGGCGGANNFRTIEBKSTCA 83
DB 61 YGGCGGANNFRTIEBKSTCA 83
RESULT 2
AAV15147 standard; Protein; 83 AA.
XX
XX AAV15147;
AC
XX 07-FEB-2000 (first entry)
DT
XX
XX Proform of Txln 3 protein.
DE
XX
XX Textillinin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
OS
XX
XX Key Location/Qualifiers
XX 1..24
XX Peptide /label= leader_peptide
XX Protein 25..83
XX /label= Txln-3_protein
XX /note= "Textillinin-3"
XX
XX MO9958569-A1.

```

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XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-AU00343.
PE
XX
XX 11-MAY-1998; 98AU-0003450.
FR
XX
XX (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASI P P.
PA (LAVI/) LAVIN M P.
PA (GAF/) GAFNEY P J.
PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
DR N-PSDB; AAZ29026.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Claim 40c; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textillinin protein, Txln 3,
CC that is a single stage competitive inhibitor of plasmin. It is isolated
CC from the Australian brown snake, Pseudonaja textilis textilis. It has
CC six conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln has high
CC specificity for plasmin and low inhibitory efficiency, that can
CC transiently affect the delicate balance between enzymes and inhibitors
CC of the fibrinolytic system, controlling the fluidity of blood. The
CC plasmin inhibitors are useful for alleviating blood loss, following
CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC propensity to cause thrombosis.
XX
XX Sequence 83 AA;
SQ
Query Match 81.2%; Score 372; DB 21; Length 83;
Best Local Similarity 79.5%; Pred. No. 1.3e-37;
Matches 66; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 1 MSSGGILLLLGLLTMEVLTTPVSSKDRHPFCELPAETGSCKGNVPRFYNNADHOCLEKI 60
DB 1 MSSGGILLLLGLLTMEVLTTPVSSKDRHPFCELPAETGSCNKKIPRFYNNPROHCIEFL 60
QY 61 YGGCGGANNFRTIEBKSTCA 83
DB 61 YGGCGGANNFRTIEBKSTCA 83
RESULT 3
AAV15141 standard; Protein; 59 AA.
XX
XX AAV15141;
AC
XX 07-FEB-2000 (first entry)
DT
XX
XX Txln 4 plasmin inhibitor protein.
DE
XX
XX Textillinin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
OS
XX
XX MO9958569-A1.
XX
XX 18-NOV-1999.

```

```

XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFV/) GAFNEY P J.
XX
XX Masi PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29020.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 8d; Page 69; 112pp; English.
XX
XX The present sequence is the Textilinin protein, Txln 4, that is a
XX single stage competitive inhibitor of plasmin. It is isolated from the
XX Australian brown snake, Pseudonaja textilis textilis. It has six
XX conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 59 AA;
SQ
Query Match 74.7%; Score 342; DB 21; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.9e-34;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 KDHKFCFLPMTSGCKGNVPRFYTNADHQCCKFYGGCGGNANFTIEGKSTCA 83
Db 1 KDHKFCFLPMTSGCKGNVPRFYTNADHQCCKFYGGCGGNANFTIEGKSTCA 59
RESULT 4
ID AAY15145 standard; Protein; 83 AA.
XX
XX AAY15145;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 1 protein.
XX
XX Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
XX haematopoietic; cytostatic activity; homology; specificity; control;
XX Talcotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX Protein /label= Leader peptide
XX /label= Txln-1 protein
XX /note= "Textilinin-1"
XX
XX MO9958569-A1.

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XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFV/) GAFNEY P J.
XX
XX Masi PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29024.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40a; Page 71; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 1,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
XX 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
XX
XX Sequence 83 AA;
SQ
Query Match 74.5%; Score 341; DB 21; Length 83;
Best Local Similarity 77.1%; Pred. No. 7.7e-34;
Matches 64; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 1 MSSGGLILLGLITMEVLTTPVSSKDHKFCFLPMTSGCKGNVPRFYTNADHQCCKFY 60
Db 1 MSSGGLILLGLITMEVLTTPVSSKDHKFCFLPMTSGCKGNVPRFYTNADHQCCKFY 60
QY 61 YGCGGNANFTIEGKSTCA 83
Db 61 YGCGGNANFTIEGKSTCA 83
RESULT 5
ID AAY15146 standard; Protein; 83 AA.
XX
XX AAY15146;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 2 protein.
XX
XX Textilinin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
XX haematopoietic; cytostatic activity; homology; specificity; control;
XX Talcotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX
XX OS
XX
XX
XX
XX

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FT Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-2_protein
FT /note= "Textilinin-2"
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNITV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.
XX
XX Maaci PP, Lavin MF, Gaffney PJ, Sorokina NI, Philippovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229025.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40b; Page 71; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 2,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln 2 has 43% and
XX 55% homology with Aprotinin and Talcotxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency, that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 72.7%; Score 333; DB 21; Length 83;
XX Best Local Similarity 74.7%; Pred. No. 7.3e-33;
XX Matches 62; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGILLILGLTTMEVLTTPVSSKDPKPCFCELPATGSGCKGNVPFFYNADHHQCLKFI 60
XX Db 1 MSSGGILLILGLTTMEVLTTPVSSKDPKPCFCELPATGSGCKGNVPFFYNADHHQCLKFI 60
XX
XX QY 61 YGGCGGNANNPFTKEGKSTCA 83
XX Db 61 YGGCGGNANNPFTKEGKSTCA 83
XX
XX RESULT 6
XX ID AAY15149
XX AAY15149 standard; Protein; 83 AA.
XX
XX AAY15149;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 5 protein.
XX
XX Textilinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX

```

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XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /label= Leader_peptide
XX FT Protein 25..83
XX FT /label= Txln-5_protein
XX FT /note= "Textilinin-5"
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNITV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.
XX
XX Maaci PP, Lavin MF, Gaffney PJ, Sorokina NI, Philippovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229028.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40e; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 5,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 69.2%; Score 317; DB 21; Length 83;
XX Best Local Similarity 72.3%; Pred. No. 6.6e-31;
XX Matches 60; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGILLILGLTTMEVLTTPVSSKDPKPCFCELPATGSGCKGNVPFFYNADHHQCLKFI 60
XX Db 1 MSSGGILLILGLTTMEVLTTPVSSKDPKPCFCELPATGSGCKGNVPFFYNADHHQCLKFI 60
XX
XX QY 61 YGGCGGNANNPFTKEGKSTCA 83
XX Db 61 YGGCGGNANNPFTKEGKSTCA 83
XX
XX RESULT 7
XX ID AAY15150
XX AAY15150 standard; Protein; 83 AA.
XX
XX AAY15150;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 6 protein.
XX

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XX XX Textilin protein; Txln 6; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KM reduced propensity; thrombosis;
XX XX
OS Pseudonaja textilis textilis.
XX XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader peptide
FT Protein 25..83
FT /label= Txln-6 protein
FT /note= "Textilinin-6"
XX XX
XX MO958569-A1.
XX PD 18-NOV-1999.
XX PP 07-MAY-1999; 99WO-AU00343.
XX PR 11-MAY-1998; 98AU-0003450.
XX XX
XX (UYOU ) UNIV QUEENSLAND.
XX PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX PA (MASC/) MASC P P.
XX PA (LAVI/) LAVIN M F.
XX PA (GAFF/) GAFFNEY P J.
XX XX
XX Maeci PE, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,
XX DR WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29029.
XX XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX PT
XX Claim 40f; Page 72; 112pp; English.
XX XX
XX The present sequence is the proform of the Textilin protein, Txln 6,
XX CC that is a single stage competitive inhibitor of plasmin. It is isolated
XX CC from the Australian brown snake, Pseudonaja textilis textilis. It has
XX CC six conserved cysteine residues, that endow them great stability. This
XX CC sequence has haematopoietic and cytostatic activity. Txln has high
XX CC specificity for plasmin and low inhibitory efficiency, that can
XX CC transiently affect the delicate balance between enzymes and inhibitors
XX CC of the fibrinolytic system, controlling the fluidity of blood. The
XX CC plasmin inhibitors are useful for alleviating blood loss, following
XX CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX CC propensity to cause thrombosis.
XX XX
XX Sequence 83 AA;
SQ
XX
XX Query Match 67.2%; Score 308; DB 21; Length 83;
XX Best Local Similarity 69.9%; Pred. No. 8,2e-30;
XX Matches 58; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
XX
XX 1 MSSGGILLILGLITLMEVLTVPVSSKHDKPCFLPABTSSCKGNVRFYNNADHQCIAFI 60
XX 1 MSSGGILLILGLITLMEVLTVPVSSKHDKPCFLPADIGPWMDFTGAFHYSPREHCIEFI 60
XX
XX 61 YGGCGGNANPKTIRBKSTCA 83
XX ||||| ||||| : |||||
XX
XX 61 YGGCGGNANPNFTDQCESTCA 83
XX ||||| ||||| : |||||
XX
XX RESULT 8
XX ID AAY15140 standard; Protein; 59 AA.
XX XX

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AC	AAV15140;
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Txln 3 Plasmin inhibitor protein.
XX	
KW	Textillin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
KM	Australian brown snake; conserved cysteine residue; stability; control;
KM	haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
KM	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KV	fibrinolysis system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX	reduced propensity; thrombosis.
XX	
OS	Pseudonaja textilis textilis.
XX	
PN	MO9958569-A1.
PD	18-NOV-1999.
XX	
PP	07-MAY-1999; 99WO-AU00343.
PR	11-MAY-1998; 98AU-0003450.
XX	
PA	(UYOU) UNIV QUEENSLAND.
PA	(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA	(MASC/) MASC P P.
PA	(LAVI/) LAVIN W F.
PA	(GAFF/) GAFFNEY P J.
PI	Maecl PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,
DR	WPI; 2000-038073/03.
DR	N-PDB; AAZ29019.
XX	
PT	Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT	agents -
PS	
XX	Claim 8c; Page 69; 112pp; English.
CC	The present sequence is the Textillin protein, Txln 3, that is a
CC	single stage competitive inhibitor of plasmin. It is isolated from the
CC	Australian brown snake, Pseudonaja textilis textilis. It has six
CC	conserved cysteine residues, that endow them great stability. This
CC	sequence has haematopoietic and cytoskeletal activity. Txln has high
CC	specificity for plasmin and low inhibitory efficiency, that can
CC	transiently affect the delicate balance between enzymes and inhibitors
CC	of the fibrinolytic system, controlling the fluidity of blood. The
CC	plasmin inhibitors are useful for alleviating blood loss, following
CC	major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC	anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX	propensity to cause thrombosis.
SQ	
Sequence	59 AA;
Query Match	55.9%; Score 256; DB 21; Length 59;
Best Local Similarity	71.2%; Pred. No. 1.2e-23;
Matches	42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Dy	
25	KDHPKFEELPAETGSCCKGNVPFRFYADHDHQCLEKYTGCGGGANNRKTIEEGSTCA 83
1	KDRNFCKLPALGTGRCNAKIPRFYMDROHCIEFLYGCGGGANNRKTIKCESTCA 59
ID	AAV15151 standard; Protein; 60 AA.
XX	
AAV15151;	
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Plasmin inhibitor Txln 1, partial protein sequence.
XX	

[illegible]

Txln 1 Plasmin inhibitor protein.

Textilinin protein; Txln 1; plasmin inhibitor; single stage inhibitor; Australian brown snake; conserved cysteine residue; stability; control; haematopoietic; cytostatic activity; homology; specificity; Aprotinin; Talicoctoxin-associated plasmin inhibitor; TAC; inhibitory efficiency; fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme; fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent; reduced propensity; thrombolysis.

Pseudonaja textilis textilis.

WO9586569-A1.

18-NOV-1999.

07-MAY-1999; 99WO-AU00343.

11-MAY-1998; 98AU-0003450.

(UYOU) UNIV QUEENSLAND.
(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
(MASC/) MASI P P.
(LAVI/) LAVIN M F.
(GAFF/) GAFFNEY P J.

Maecl PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,
WPI; 2000-039073/03.
N-Psdb; AAZ29017.

Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor agents -

Claim 8a; Page 68; 112pp; English.

The present sequence is the Textilinin protein, Txln 1, that is a single stage competitive inhibitor of plasmin. It is isolated from the Australian brown snake, Pseudonaja textilis textilis. It has six conserved cysteine residues, that endow them great stability. This sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and 58% homology with Aprotinin and Talicoctoxin-associated plasmin inhibitor (TAC), respectively. Txln has high specificity for plasmin and low inhibitory efficiency, that can transiently affect the delicate balance between enzymes and inhibitors of the fibrinolytic system, controlling the fluidity of blood. The plasmin inhibitors are useful for alleviating blood loss, following major surgery or trauma. Conjugates of the plasmin inhibitor and an anti-fibrin antibody are useful as anti-tumour agents. They have reduced propensity to cause thrombolysis.

Sequence 59 AA;

Query Match 49.1%; Score 225; DB 21; Length 59;
Best Local Similarity 67.8%; Pred. No. 7.4e-20;
Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0.

25 KDRKFCLEPALTGSCSKGNVRPFYFNADHQCLEFYIGCGGANNFTEEGSTCA 83
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
1 KDRDFCGLPADTGPCRVRFSPFYFNDEKKCLEFYIGCGGANNFITKECESTCAA 59

RESULT 11
AAV15153
ID AAV15153 standard; Protein; 60 AA.

AAV15153;
07-FEB-2000 (first entry)

Plasmin Inhibitor Txln 1, encoded by partial cDNA sequence.

Textilinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;


```

OS Synthetic.
PN MO9620278-A2.
PD 04-JUL-1996.
XX
XX
PP 15-DEC-1995; 95WO-US16349.
XX
XX PR 16-DEC-1994; 94US-0358160.
XX
XX PA (PROT-) PROTEIN ENG CORP.
XX
XX PI Guerman SK, Kent RB, Lachner RC, Ley AC, Markland W;
XX Roberge BL;
XX WP1; 1996-321851/32.
XX
XX PT New engineered inhibitors of human neutrophil elastase - contg.
XX PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
XX PT other respiratory disorders
XX
XX PS Example 23; Page 47; 105pp; English.
XX
XX CC Genetically engineered human derived Kunitz domains can be used to
XX CC inhibit human neutrophil elastase, an enzyme involved in the
XX CC elimination of pathogens and the restructuring of connective tissue.
XX CC In cases of reduction of the circulating alpha-1-protease inhibitor
XX CC (API or alpha antitrypsin), or the inactivation of API by oxidation
XX CC (smokers emphysema), extensive destruction of the lung tissue may
XX CC result from uncontrolled elastolytic activity of human neutrophil
XX CC elastase. Other respiratory disorders such as cystic fibrosis are
XX CC thought to be caused by human neutrophil elastase release by
XX CC neutrophils. The genetically engineered human derived Kunitz
XX CC domains can be used to treat such respiratory disorders. See
XX CC AA899146-R99211.
XX
XX SQ Sequence 58 AA;
XX
XX Query Match 46.1%; Score 211; DB 17; Length 58;
XX Best Local Similarity 68.5%; Pred. No. 3,7e-18;
XX Matches 37; Conservative 4; Mismatches 13; Indels 0; Gaps 0
XX
OY 28 PKECELPAETGSCCKENVRPRFYTNADHGOCLKRTYGGCGGNANFTIBGKSTC 81
XX | | | | | : | | | | | : | | | | | : | | | | | : | |
XX | | | | | : | | | | | : | | | | | : | | | | | : | |
D6 2 PDFCLPAPETGCPRAMIPRFYNNAXSGKCEPRYGGCGGNANFTIBECRCSTC 55
XX
RESULT 14
XX ID AAY15142 standard; Protein; 59 AA.
XX AAY15142
XX AAY15142;
XX
XX DT 07-FEB-2000 (first entry)
XX
XX TX1n 5 Plasmin inhibitor protein.
XX
XX Textilinin protein; TX1n 5; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX OS Pseudonaja textilis textilis.
XX
XX WO9958569-A1.
XX
XX PD 18-NOV-1999.
XX
XX PP 07-MAY-1999; 99WO-AU00343.
XX
XX PR 11-MAY-1998; 98AU-0003450.
XX

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(UNIV QUEENSLAND.
NAB(-) NAT INST BIOLOGICAL STANDARDS & CO.
(MASC/) MASC P P.
(LAVI/) LAVIN M F.
(GAF/) GAFNEY P J.

Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
WPI; 2000-039073/03.
DR N-PSDB; AA229021.

Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
agents -
Claim 8e; Page 69; 112pp; English.

The present sequence is the Textillin protein, Txln 5, that is a
single stage competitive inhibitor of plasmin. It is isolated from the
Australian brown snake, Pseudonaja textilis textilis. It has six
conserved cysteine residues, that endow them great stability. This
sequence has haematopoietic and cytostatic activity. Txln has high
specificity for plasmin and low inhibitory efficiency, that can
transiently affect the delicate balance between enzymes and inhibitors
of the fibrinolytic system, controlling the fluidity of blood. The
plasmin inhibitors are useful for alleviating blood loss, following
major surgery or trauma. Conjugates of the plasmin inhibitor and an
anti-fibrin antibody are useful as anti-tumour agents. They have reduced
propensity to cause thrombosis.

Sequence 59 AA:

Query Match 43.9%; Score 201; DB 21; Length 59;
Best Local Similarity 61.0%; Pred. No. 6.3e-17;
Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

25 KDHKKPEELPAEFGSCCKGNVPRFYNNADHHQCKETIGGGCGGANNFKTIEEGKSTCA 83
Db 1 KDRPKFELLPPDTGSCDEFTGAFFYSTRDRBCLEFFITGGCGGANNPTIRECESTCA 59

RESULT 15
AA15154
ID AA15154 standard; Protein; 60 AA.
XX AC
XX AAY15154;
XX XX
XX 07-FEB-2000 (first entry)
XX DE
XX Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
XX DE
XX Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytostatic activity; homology; enzyme;
KW fluidity of blood; alleviate; blood loss; major surgery; trauma;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX inhibitory efficiency; reduced propensity; thrombosis.
XX OS
XX Pseudonaja textilis textilis.
XX XX
XX Key Location/Qualifiers
FH Misc-difference 24 /note= "encoded by TTG"
FT FT
FT Misc-difference 45 /note= "encoded by GAT"
FT FT
FT Misc-difference 49 /note= "encoded by ATG"
FT Misc-difference 59 /note= "encoded by CCN"
XX XX
XX MO9958569-A1.
XX PD 18-NOV-1999.

```

XX 07-MAY-1999; 99WO-AU00343.
PF
XX
PR 11-MAY-1998; 98AU-0003450.
XX
PA (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASI P P.
PA (LAVI/) LAVIN M F.
PA (GAFNEV) GAFNEV P J.
PI Masi PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29048.
XX
PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
agents -
XX
PS Disclosure; Fig 7; 112pp; English.
XX
CC The present amino acid sequence is the Txln 2, Textilinin protein
CC encoded by the partial cDNA sequence. It is a single stage competitive
CC inhibitor of plasmin. It is isolated from the Australian brown snake,
CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
CC low inhibitory efficiency that can transiently affect the delicate
CC balance between enzymes and inhibitors of the fibrinolytic system,
CC controlling the fluidity of blood. The plasmin inhibitors are useful for
CC alleviating blood loss, following major surgery or trauma. Conjugates of
CC the plasmin inhibitor and an anti-fibrin antibody are useful as
CC anti-tumour agents. They have reduced propensity to cause thrombosis.
XX
SQ Sequence 60 AA:
Query Match 42.1%; Score 193; DB 21; Length 60;
Best Local Similarity 59.6%; Pred. No. 6.1e-16;
Matches 34; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
QY 25 KDHPKPCFLPAETGSCCKGNVPRFYNNADHOCLEKPIYGGCGGNANNFKTIERGKSTC 81
DB 2 KDRPELCFLPPDTGFCRVRFPSPFYNNPDQKLEFIYGGCEBNANAFITKBECESTC 58

```

Search completed: January 23, 2004, 10:24:36
 Job time : 40.0387 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 7.59859 Seconds
(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179A-16

Sequence: 1 MSQGGILLGLITLMEVLT.....CEGNANNTKECESTCAA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	49.9	85	1	IVB2_BUNMU
2	214	46.8	65	1	IVB3_VITPA
3	204	44.6	62	1	IP52_ANESU
4	201	44.0	57	1	IVB2_NAJNI
5	201	44.0	61	1	IVB1_VITPA
6	198	43.3	57	1	IVB2_HEMAA
7	195	42.7	62	1	IVBT_HERMA
8	195	42.7	85	1	IVBT_BUNMU
9	194	42.5	57	1	IVBT_NAJNA
10	192	42.0	65	1	IVB1_BUNPA
11	189	41.4	110	1	IBP_GARCR
12	188.5	41.2	230	1	TPP2_MOUSE
13	188	41.1	58	1	ISIK_HELPO
14	187.5	41.0	55	1	SEPTI_BOMMO
15	180	39.4	252	1	SEPTI_HUMAN
16	179	39.2	58	1	AXPI_ANTAF
17	179	39.2	59	1	IVBB_DENPO
18	178	38.9	60	1	IVB2_DABRU
19	172	37.6	302	1	TPPI_RAT
20	171	37.4	300	1	TPPI_RABIT
21	171	37.4	306	1	TPPI_MOUSE
22	170.5	37.3	122	1	UPPI_PIG
23	170	37.2	235	1	TPP2_HUMAN
24	169	37.0	57	1	IVBK_DENAN
25	169	37.0	304	1	TPPI_MACMU
26	168	36.8	57	1	IVBK_DENPO
27	168	36.8	58	1	IVBC_OPHHA
28	168	36.8	133	1	BPTI_HUMAN
29	167	36.5	58	1	AXP2_ANTAF
30	166.5	36.4	100	1	BPTI_BOVIN
31	166	36.3	513	1	SBPI_HUMAN
32	165	36.1	57	1	SBPI_SARBU
33	163.5	35.8	100	1	BPT2_BOVIN

34	163	35.7	252	1	SPT2_MOUSE	O9WU03 mus musculus
35	162.5	35.6	69	1	CRPT_BOOMI	P81162 boophilus m
36	162	35.4	304	1	TPPI_HUMAN	P10646 homo sapien
37	160	35.0	3176	1	CA36_HUMAN	P12111 homo sapien
38	153	33.5	57	1	IVBB_DENPO	P00983 dendroaspis
39	152	33.3	60	1	IBPS_BOVIN	P00975 bos taurus
40	152	33.3	770	1	A4_MOUSE	P12023 m amyloid b
41	151	33.0	507	1	SPT1_MOUSE	O9T097 mus musculus
42	150.5	32.9	352	1	AMB_P_HUMAN	P02760 homo sapien
43	150	32.8	76	1	A4_MACMU	P29216 macaca mula
44	150	32.8	751	1	A4_SAISC	O95241 s amyloid b
45	150	32.8	770	1	A4_HUMAN	P05067 h amyloid b

ALIGNMENTS

RESULT 1
ID IVB2_BUNMU STANDARD, PRT; 85 AA.
AC P00989; O42299; Q9PRV8; Q9PTA3;
DT 21-JUL-1986 (Ref. 01, Created)
DT 15-JUL-1998 (Ref. 36, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Beta bungarotoxin B2 chain precursor.
OS Bungarus multicinctus (Many-banded Krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosteia; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
CN NCBI_TaxID=8616;
NM (1)
NM SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=98359733; PubMed=9693106;
RA Wu P.-F., Chang L.-S.;
RT "Cloning and functional expression of B chains of beta-bungarotoxins
from Bungarus multicinctus (Taiwan banded Krait).";
RL Biochem. J. 334:87-92(1998).
NM (2)
NM SEQUENCE OF 1-82 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20363696; PubMed=10903499;
RA Wu P.-F., Chang L.-S.;
RT "Genetic structures of A chain and B chain of beta-bungarotoxin from
Taiwan banded krait (Bungarus multicinctus). A chain genes and B chain
genes do not share a common origin.";
RL Eur. J. Biochem. 267:4668-4675(2000).
NM (3)
NM SEQUENCE OF 25-85.
RC TISSUE=Venom;
RX MEDLINE=82239269; PubMed=7096304;
RA Kondo K., Toda H., Narita K., Lee C.-Y.;
RT "Amino acid sequence of beta 2-bungarotoxin from Bungarus
multicinctus venom. The amino acid substitutions in the B chains.";
RL J. Biochem. 91:1519-1530(1982).
NM (4)
NM SEQUENCE OF 25-63.
RC MEDLINE=95031955; PubMed=7945237;
RA Chu C.C., Chu S.T., Chen S.W., Chen Y.H.;
RT "The non-phospholipase A2 subunit of beta-bungarotoxin plays an
important role in the phospholipase A2-independent neurotoxic effect:
RT characterization of three isoforms with a common phospholipase A2
subunit.";
RL Biochem. J. 303:171-176(1994).
NM (5)
NM REVIEWS.
RX MEDLINE=20396379; PubMed=10936627;
RA Rowan B.G.;
RT "What does beta-bungarotoxin do at the neuromuscular junction?";
RL Toxicon 39:107-118(2001).
CC -1- FUNCTION: Beta-2 bungarotoxin is a presynaptic neurotoxin of the
venom. The B chain is homologous to venom basic protease
inhibitors but has no protease inhibitor activity and is non-

```

CC      toxic.
CC      -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
CC      The A chains have phospholipase A2 activity and the B chains show
CC      homology with the basic protease inhibitors.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y12101; CAI72810.1; -.
DR      EMBL; AJ251224; CAB62504.1; -.
DR      PDB; 1BUN; 03-APR-96.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF00014; Kunitz_BPTI_1.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Toxin; Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
FT      SIGNAL          1      24
FT      CHAIN           25      85
FT      DOMAIN          31      81
FT      DISULFID        31      81
FT      DISULFID        40      64
FT      DISULFID        56      77
FT      DISULFID        79      79
FT      ACT_SITE        41      42
FT      CONFLICT        44      44
FT      CONFLICT        65      70
FT      CONFLICT        82      83
FT      CONFLICT        82      83
SQ      SEQUENCE      85 AA; 9568 MW; FE95A59AF92B2AA CRC64;

Query Match          49.9%; Score 228; DB 1; Length 85;
Best Local Similarity 54.3%; Pred. No. 2.2e-19;
Matches 44; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

Cy      1 MSSGGILLILGILTLMTLVTPSSKDRPFGLPADTGRCRRPFSFYNPBEKCLERF 60
Db      1 MSSGGILLILGILTLCAELTPVSSRRKHPDCRPPDTKICQTVRAFYKPSAKGVQPR 60

Cy      61 YGGCEGNANNPFTKEECSTC 81
Db      61 YGGCNGNGNHPKSDHLCRCEC 81

RESULT 2
IVB3_VIPAA STANDARD; PRT; 65 AA.
AC      P00952;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DR      Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
OS      Vipera ammodytes ammodytes (Western sand viper).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Viperidae; Viperinae; Vipera.
OX      NCBI_TaxID=8705;
OC      [1]
SQ      SEQUENCE.
RP      Tissue=Venom;
RA      Riconja A., Meloun B., Gubensek F.;
RT      "The primary structure of Vipera ammodytes venom chymotrypsin
RT      inhibitor.";
RL      Biochim. Biophys. Acta 746:138-145(1983).
CC      -1- FUNCTION: This protein inhibits chymotrypsin.

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CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR      PIR; A01223; TIVYC.
DR      HSSP; P31713; ISHP.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF00014; Kunitz_BPTI_1.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Serine protease inhibitor.
FT      DISULFID        7      57
FT      DISULFID        16      40
FT      DISULFID        32      53
FT      ACT_SITE        17      18
SQ      SEQUENCE      65 AA; 7556 MW; 9D526F83BF7C57 CRC64;

Query Match          46.8%; Score 214; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 6.6e-18;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy      25 KDRPFGLPADTGRCRRPFSFYNPBEKCLERFYGGCEGNANNPFTKEECSTCA 83
Db      1 RDRPFGLPADTGRCRRPFSFYNPBEKCLERFYGGCEGNANNPFTKEECSTCA 59

RESULT 3
IP52_ANESU STANDARD; PRT; 62 AA.
AC      P10280;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DR      Protease inhibitor 5 II (SAs II).
OS      Anemona sulcata (Snake-larks sea anemone).
OC      Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;
OC      Nymphaeae; Actinellidae; Anemonta.
OX      NCBI_TaxID=6108;
RN      [1]
RP      SEQUENCE OF 1-59.
RA      Wunderer G., Machleidt W., Fritze H.;
RT      "The broad-specificity proteinase inhibitor 5 II from the sea anemone
RT      Anemona sulcata.";
RL      Meth. Enzymol. 80:816-820(1981).
RN      [2]
RP      SEQUENCE.
RA      Krebs H.C., Habermehl G.G.;
RT      "Isolation and structural determination of a hemolytic active peptide
RT      from the sea anemone Metridium senile.";
RL      Naturwissenschaften 74:395-396(1987).
CC      -1- FUNCTION: INHIBITOR OF KALLIKREINS.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      PIR; S07451; S07451.
DR      HSSP; P31713; ISHP.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF00014; Kunitz_BPTI_1.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Serine protease inhibitor.
FT      DISULFID        5      55
FT      DISULFID        14      38
FT      DISULFID        30      51
FT      ACT_SITE        15      16
FT      VARIANT         13      13
FT      VARIANT         16      16
FT      VARIANT         17      17
FT      VARIANT         17      17
FT      VARIANT         25      25
FT      VARIANT         28      28
FT      VARIANT         39      39
SQ      SEQUENCE      62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

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Query Match 44.6%; Score 204; DB 1; Length 62;
 Best Local Similarity 66.7%; Pred. No. 8.8e-17;
 Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 31 CELPADTGCRVAFPSFYTNPEDEKCLFEFYGGCGGNANFTKECESTC 81
 Db 5 CELPKVGCRAFPFRYYNSSSKCEKFIYGGCGGNANFTLECEKVC 55

RESULT 4
 IVB2_NAJNI STANDARD; PRT; 57 AA.
 AC P00986;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Naja naja (Cape cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Naja.
 NCBI_TaxID=8655;
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Rhinhal's corbra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them."
 RT J. Biochem. 79:559-578(1976).
 RL FUNCTION: The activity of this inhibitor is probably similar to
 CC -1- FUNCTION: The activity of this inhibitor is probably similar to
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01217; TINTVC.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 44.0%; Score 201; DB 1; Length 57;
 Best Local Similarity 63.6%; Pred. No. 1.8e-16;
 Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RPDPCELPADTGCRVAFPSFYTNPEDEKCLFEFYGGCGGNANFTKECESTC 81
 Db 1 RPRFCLEPAPVGCRAFPFRYYNSSSKCEKFIYGGCGGNANFTLECEKVC 55

RESULT 5
 IVB1_VIPAA STANDARD; PRT; 61 AA.
 AC P00981;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor I (Venom trypsin inhibitor I).
 OS Viperinae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Viperinae.

OX NCBI_TaxID=8705;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=84053385; PubMed=6639951;
 RA Ritorja A., Meloun B., Gudensnek F.;
 RT "The primary structure of Viperinae venom trypsin inhibitor
 RT I."
 RL Biochim. Biophys. Acta 748:429-435(1983).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01222; TIVT1.
 DR HSSP; P31713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Pyroliidone carboxylic acid.
 FT MOD_RES 1 1 PYROLIIDONE CARBOXYLIC ACID.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 SQ SEQUENCE 61 AA; 6865 MW; FC8285F579FE3795 CRC64;

Query Match 44.0%; Score 201; DB 1; Length 61;
 Best Local Similarity 57.6%; Pred. No. 1.9e-16;
 Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 25 KDRPDCLEPADTGCRVAFPSFYTNPEDEKCLFEFYGGCGGNANFTKECESTCA 83
 Db 1 QDRPKCYLPADTGCRVAFPSFYTNPEDEKCLFEFYGGCGGNANFTLECEKVC 59

RESULT 6
 IVB2_HEMHA STANDARD; PRT; 57 AA.
 AC P00985;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Rhinhal's corbra) (Sepsodon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Hemachatus.
 NCBI_TaxID=8626;
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Rinhal's corbra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them."
 RT J. Biochem. 79:559-578(1976).
 RL FUNCTION: The activity of this inhibitor is similar to that of
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01216; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.

FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7F2A CRC64;
 Query Match 43.3%; Score 198, DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 3.9e-16;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 27 RPDCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTC 81
 DB 1 RPDCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTC 55
 RESULT 7
 ID IVBT_ERIMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis macmahoni (Leaf-nosed viper).
 OC Bufoyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Eristocophis.
 OC NCBI_Taxid=8702;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 from leaf-nosed viper venom."
 RL FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC PIR: S19327; S19327.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 2 52 BY SIMILARITY.
 FT DISULFID 11 35 BY SIMILARITY.
 FT DISULFID 27 48 BY SIMILARITY.
 FT ACT SITE 12 13 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;
 Query Match 42.7%; Score 195; DB 1; Length 62;
 Best Local Similarity 61.1%; Pred. No. 9.5e-16;
 Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;
 QY 30 RCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTCA 83
 DB 1 RCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTCA 54
 RESULT 8
 ID IVBT_BUNMU STANDARD; PRT; 85 AA.
 AC P00987; O42298; P00988;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta bungarotoxin B1 chain, major component precursor.
 OS Bungarus multicinctus (Many-banded krait).
 OC Bufoyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Bungarinae; Bungarus.
 OC NCBI_Taxid=8616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=98359733; PubMed=9693106;
 RA Wu P.-F., Wu S.-N., Chang C.-C., Chang L.-S.;
 RT "Cloning and functional expression of B chains of beta-bungarotoxins
 from Bungarus multicinctus (Taiwan banded krait)."
 RL Biochem. J. 334:87-92(1998).
 RN [2]
 RP SEQUENCE OF 25-85.
 RC TISSUE=Venom;
 RX MEDLINE=78109400; PubMed=624701;
 RA Kondo K., Narita K., Lee C.-Y.;
 RT "Amino acid sequences of the two polypeptide chains in beta1-
 bungarotoxin from the venom of Bungarus multicinctus."
 RL J. Biochem. 83:101-115(1978).
 RN [3]
 RP MUTAGENESIS OF CYS-32.
 RX MEDLINE=21589307; PubMed=11732693;
 RA Wu P.-F., Chang L.-S.;
 RT "Expression of A chain and B chain of beta-bungarotoxin from taiwan
 banded krait: the functional implication of the interchain disulfide
 bond between A chain and B chain."
 RL J. Protein Chem. 20:413-421(2001).
 RN [4]
 RP REVIEW.
 RX MEDLINE=20396379; PubMed=10936627;
 RA Roman B.G.;
 RT "What does beta-bungarotoxin do at the neuromuscular junction?"
 RL Toxicol 39:107-118(2001).
 CC -1- FUNCTION: Beta-1 bungarotoxin is a presynaptic neurotoxin of the
 venom. The B chain is homologous to venom basic protease
 inhibitors, but has no protease inhibitor activity and is non-
 toxic.
 CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
 CC The A chains have phospholipase A2 activity and the B chains show
 homology with the basic protease inhibitors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; Y12100; CAA72809.1; -.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Toxin; Neurotoxin; Presynaptic neurotoxin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 85
 FT DOMAIN 31 81
 FT DISULFID 31 81 BPTI/KUNITZ INHIBITOR.
 FT DISULFID 40 64 BY SIMILARITY.
 FT DISULFID 56 77 BY SIMILARITY.
 FT DISULFID 79 79 INTERCHAIN (WITH AN A CHAIN).
 FT ACT SITE 41 42 REACTIVE BOND (BY SIMILARITY).
 FT MUTAGEN 79 79 C->S; LOSS OF PA2 ACTIVITY. WEAK LOSS IN
 FOLDING.
 FT MISSING (IN REF. 2).
 FT CONFLICT 45 45 NNGNHN -> DDDHGN (IN REF. 2).
 FT SEQUENCE 85 AA; 9571 MW; A1E3D452A67DE5C CRC64;

Query Match 42.7%; Score 195; DB 1; Length 85;
 Best Local Similarity 51.9%; Pred. No. 1.3e-15;
 Matches 42; Conservative 6; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSGGGLLLGLTLTMEVLTPVSSKDRPDPFCELPADTGPCRVPPSPFYNDPDEKCKLEFI 60
 DB 1 MSGGGLLLGLTLTLCABELPVSRSORHRDCDPPDKMCGPVARAFYDTRLTCTCAFO 60
 QY 61 YGCGEGNANPITKEBCESTC 81
 DB 61 YRGCGNGNHFXTETLCRCRC 81

RESULT 9
 IYBT_NAJNA STANDARD; PRT; 57 AA.
 AC P20229;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Naja.
 NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=9109304; PubMed=1702708;
 RA Shafqat J., Beg O.U., Yin S.-J., Zaidi Z.H., Joernvall H.;
 RT "Primary structure and functional properties of cobra (Naja naja
 RT naja) venom Kunitz-type trypsin inhibitor."; B.M.J. Biochem. 194;337-341(1990).
 RL -1- FUNCTION: This protein inhibits trypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P00981; 1DTX.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6371 MW; AABFD72949ADC12A CRC64;

Query Match 42.5%; Score 194; DB 1; Length 57;
 Best Local Similarity 60.0%; Pred. No. 1.1e-15;
 Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 27 RPPDFCELPADTGPCRVPPSPFYNDPDEKCKLEFIYGGCGNANPITKEBCESTC 81
 DB 1 RPPDFCELPADTGPCRVPPSPFYNDPDEKCKLEFIYGGCGNANPITKEBCESTC 81

RESULT 10
 IYBI_BUNFA STANDARD; PRT; 65 AA.
 AC P25660;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitors IX and VIIIB.
 OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 NCBI_TaxID=8613;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=83160048; PubMed=6832893;
 RA Liu C.-S., Wu T.-C., Lo T.-B.;
 RT "Complete amino acid sequences of two protease inhibitors in the
 RT venom of Bungarus fasciatus."; Int. J. Pept. Protein Res. 21;209-215(1983).
 RL Int. J. Pept. Protein Res. 21;209-215(1983).
 CC -1- FUNCTION: Inhibitor of chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P00980; 1DTX.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 7 57 BY SIMILARITY.
 FT DISULFID 16 40 BY SIMILARITY.
 FT DISULFID 32 53 BY SIMILARITY.
 FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
 FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).
 SQ SEQUENCE 65 AA; 7294 MW; BA340749B194DB51 CRC64;

Query Match 42.0%; Score 192; DB 1; Length 65;
 Best Local Similarity 57.6%; Pred. No. 2.2e-15;
 Matches 34; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 25 KDRPFCLEPADTGPCRVPPSPFYNDPDEKCKLEFIYGGCGNANPITKEBCESTCA 83
 DB 1 KDRPFCLEPADTGPCRVPPSPFYNDPDEKCKLEFIYGGCGNANPITKEBCESTCA 59

RESULT 11
 IYB_CARCR STANDARD; PRT; 110 AA.
 AC P00993;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chelonanthin (Basic protease inhibitor) (RTPI).
 OS Chelonanthin (Basic protease inhibitor).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Chelonioidea; Cheloniidae; Caretta.
 NCBI_TaxID=8467;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Egg white;
 RA Kato I., Tomioka N.;
 RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists
 RT of two tandem domains -- one Kunitz -- one of a new family."; J. Biol. Chem. 263;832-832(1979).
 RL Red. Proc. 38;832-832(1979).
 CC -1- FUNCTION: THE FIRST DOMAIN INHIBITS TRYPSIN; THE SECOND ONE
 CC INHIBITS SUBTILISIN.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -1- SIMILARITY: Contains 1 WAP-type domain.
 CC -1- TURTLE: AS THE PAPER ONLY INDICATES THE SPECIES AS "RED SEA
 CC TURTLE", THE SPECIES INDICATED HERE IS THEREFORE AN INFERENCE.
 DR PIR; A01224; TITR.
 DR HSSP; P00974; 6PTI.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor; Pyrolydone carboxylic acid.
 FT DOMAIN 8 58 BPTI/KUNITZ INHIBITOR.
 FT MOD_RES 63 105 WAP.
 FT DISULFID 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 17 58 BY SIMILARITY.
 FT DISULFID 33 54 BY SIMILARITY.
 FT DISULFID 67 92 BY SIMILARITY.
 FT DISULFID 76 97 BY SIMILARITY.
 FT DISULFID 80 93 BY SIMILARITY.
 FT DISULFID 86 101 BY SIMILARITY.
 FT ACT_SITE 18 19 REACTIVE BOND (TRYPSIN).
 SQ SEQUENCE 110 AA; 11916 MW; 2694362438134188 CRC64;
 Query Match 41.4%; Score 189; DB 1; Length 110;
 Best Local Similarity 53.6%; Pred. No. 8.4e-15;
 Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 26 DRDPFCELPADTGPCRVFPSPFTYNPDEKCLPFIYGGCBGNANFTKECESTC 81
 Db 3 DKRDICRLPFGPGCKGRIPRYFYNPAPSMCESPFYGGCKGNKNNFKTKACGVRA 58
 RESULT 12
 TF22 MOUSE STANDARD; PRT; 230 AA.
 ID TF22 MOUSE STANDARD; PRT; 230 AA.
 AC O3536;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
 GN TFPI2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97101108; PubMed=8945635;
 RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,
 Itoh H., Hori T., Aoki I., Mitsu K., Miyazaki K.;
 RT "Cloning of the cDNA encoding mouse PPS/TFPI-2 and mapping of the gene
 to chromosome 6.";
 RT DNA Cell Biol. 15:947-954(1996).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=20132652; PubMed=10669168;
 RA Kasama Y., Kamei S., Kuiper J.L., Foster D.C., Kjaer W.;
 RT "Nucleotide sequence of the gene encoding murine tissue factor pathway
 inhibitor-2.";
 RT Thromb. Haemost. 83:141-147(2000).
 RL [1]
 CC -1- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
 WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA. ALSO EXPRESSED
 IN LIVER AND KIDNEY.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- SWITLAKITY: Contains 3 BPTI/Kunitz inhibitor domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC EMBL; D50586; BA22585.1; -
 DR EMBL; AF180353; AAF40412.1; -
 DR HSPB; P12111; IKT.
 DR MSD; MG1:108543; Tfp12.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
 KM Serine protease inhibitor; Glycoprotein; Repeat; Signal;
 FT Blood coagulation.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 230 TISSUE FACTOR PATHWAY INHIBITOR 2.
 FT DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 1.
 FT DOMAIN 96 146 BPTI/KUNITZ INHIBITOR 2.
 FT DOMAIN 156 206 BPTI/KUNITZ INHIBITOR 3.
 FT ACT_SITE 46 47 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 106 107 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 166 167 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 166 167 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 35 86 BY SIMILARITY.
 FT DISULFID 45 69 BY SIMILARITY.
 FT DISULFID 61 82 BY SIMILARITY.
 FT DISULFID 96 146 BY SIMILARITY.
 FT DISULFID 105 129 BY SIMILARITY.
 FT DISULFID 121 142 BY SIMILARITY.
 FT DISULFID 156 206 BY SIMILARITY.
 FT DISULFID 165 189 BY SIMILARITY.
 FT DISULFID 181 202 BY SIMILARITY.
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 230 AA; 26137 MW; 57EAD2E36521C7B CRC64;
 Query Match 41.2%; Score 188.5; DB 1; Length 230;
 Best Local Similarity 42.7%; Pred. No. 2.1e-14;
 Matches 35; Conservative 14; Mismatches 22; Indels 11; Gaps 2;
 QY 13 LTMVEV-----LTPVSK-DRDPFCELPADTGPCRVFPSPFTYNPDEKCLPFIY 61
 Db 7 LQNNLPPLLVGSLVGLTSVBAQGNLLEICLLPDAGFCQALLPFFYDRDQCKRRFY 66
 QY 62 GCGEGNANFTKESCESTCA 83
 Db 67 GCGEGNANFTKESCESTCA 88
 RESULT 13
 ISIK HELPO STANDARD; PRT; 58 AA.
 ID ISIK HELPO STANDARD; PRT; 58 AA.
 AC P00954;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor K.
 OS Helix pomatia (Roman snail) (Edible snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
 OC Sigurethra; Helicoidea; Helicidae; Helix.
 OX NCBI_TaxID=6536;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=76043680; PubMed=1183446;
 RX Technische H., Dietl T.;
 RA "The amino-acid sequence of isoform K from snails (Helix
 pomatia). A sequence determination by automated Edman degradation and
 RT mass-spectral identification of the phenylthiohydantoin.";
 RL Eur. J. Biochem. 58:439-451(1975).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=7614310; PubMed=3462;
 RA Dietl T., Technische H.;
 RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from

RT snails (Helix pomatia). Thermal inactivation and proteolysis by
 RT chemoelastin.
 CC Hope-Sealyer's Z. Physiol. Chem. 357:139-145(1976).
 CC -1- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD
 CC SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A91232; TIRAB.
 DR HSP: P00974; 1BPI.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT_SITE 17 18
 SQ SEQUENCE 58 AA; 6451 MW; 6796586C488453B7 CRC64;
 Query Match 41.1%; Score 188; DB 1; Length 58;
 Best Local Similarity 52.7%; Pred. No. 5.6e-15;
 Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 Oy 27 RDPCELPADTGPGRVFRPSPFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 Db 3 RSPFCNLPATGTPCKASFRYYNNSKSGGQCPYGGCGGNQNRFTTCCGCGVC 57
 RESULT 14
 CSTI_BOMMO STANDARD; PRT; 55 AA.
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_Taxid=7091;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RP STRAIN=Asahi;
 RC MEDLINE=99115431; PubMed=9914483;
 RA Kurioka A., Yamazaki M., Hirano H.;
 RT "Primary structure and possible functions of a trypsin inhibitor of
 RT Bombyx mori";
 RL Eur. J. Biochem. 259:120-126(1999).
 CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
 CC Activity by forming a low-dissociation complex with trypsin. May
 CC play an important part in regulating proteolytic activity in the
 CC silk gland or protecting silk proteins from degradation during
 CC histolysis.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
 CC gland.
 CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
 CC middle silk glands during the final stage of larval growth with
 CC highest expression before the onset of spinning.
 CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
 CC -1- MICELANIZATION: Has an isoelectric point of 4.3.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR HSP: P31713; 1SHR.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Developmental protein; Serine protease inhibitor.
 FT DISULFID 4 54
 FT DISULFID 13 37
 FT DISULFID 29 50
 FT ACT_SITE 14 15
 SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2BBE59 CRC64;
 Query Match 41.0%; Score 187.5; DB 1; Length 55;
 Best Local Similarity 61.1%; Pred. No. 6.1e-15;
 Matches 33; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
 Oy 28 PDPCELPADTGPGRVFRPSPFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 Db 2 PDPCELPADTGPGRVFRPSPFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 RESULT 15
 SPT2_HUMAN STANDARD; PRT; 252 AA.
 AC Q43251; O00271; O14895; Q969E0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
 DE activator inhibitor type 2) (HAI-2) (Placental bikunin).
 GN SPTN2 OR HAI2 OR KOP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98010584; PubMed=9346890;
 RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
 RA Kitamura N.;
 RT "Purification and cloning of hepatocyte growth factor activator
 RT inhibitor type 2, a Kunitz-type serine protease inhibitor";
 RL J. Biol. Chem. 272:27558-27564(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC TISSUE=Placenta;
 RX MEDLINE=92727372; PubMed=9115294;
 RA Warior C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
 RA Tamburini P.P.;
 RT "Identification, and cloning of human placental bikunin, a novel serine
 RT protease inhibitor containing two Kunitz domains";
 RL J. Biol. Chem. 272:12202-12208(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancratic cancer;
 RX MEDLINE=98094245; PubMed=9434156;
 RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friese H.,
 RA Buechler M., Adler G., Gress T.M.;
 RT "Cloning of a new Kunitz-type protease inhibitor with a putative
 RT transmembrane domain overexpressed in pancreatic cancer";
 RL Biochim. Biophys. Acta 1395:88-95(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT LEU-200.
 RC TISSUE=Colon, and Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelli N.A., Peters S.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,
CC PLASMA AND TISSUE KALIKREIN, AND FACTOR XIA.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,
CC PROSTATE, TESTIS, THYMUS, AND TRACHEA.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL; AB006534; BAA25024.1; -.
DR EMBL; U78095; AAC02781.1; -.
DR EMBL; AF027205; AAB84031.1; -.
DR EMBL; BC001668; AAH01668.1; -.
DR EMBL; BC007705; AAH07705.1; -.
DR EMBL; BC011951; AAH11951.1; -.
DR EMBL; BC011955; AAH11955.1; -.
DR EMBL; BC012868; AAH12868.1; -.
DR HSSP; P05067; IAAI.
DR GeneW; HGNC:11247; SPINT2.
DR MIM; 605124; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0004867; F:serine protease inhibitor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW Signal; Polymorphism.
FT SIGNAL 1 27
FT CHAIN 28 252
FT DOMAIN 28 197
FT TRANSMEM 198 218
FT DOMAIN 219 252
FT DOMAIN 38 88
FT DOMAIN 133 183
FT DISULFID 38 88
FT DISULFID 47 71
FT DISULFID 63 84
FT ACT SITE 48 49
FT DISULFID 133 183
FT DISULFID 142 166
FT DISULFID 158 179
FT ACT SITE 143 144
FT CARBOHYD 57 57
FT CARBOHYD 94 94
FT VARIANT 200 200
FT CONFLICT 3 3
FT CONFLICT 11 11
FT CONFLICT 53 53
/FTid=VAR_012482.
Q -> H (IN REF. 3).
R -> P (IN REF. 1).
R -> K (IN REF. 3).

FT CONFLICT 240 240 D -> H (IN REF. 3).
SQ SEQUENCE 252 AA; 28228 MW; A7D336DC0ECB2B CRC64;
Query Match 39.4%; Score 180; DB 1; Length 252;
Best Local Similarity 43.8%; Pred. No. 2.1e-13;
Matches 35; Conservative 10; Mismatches 35; Indels 0; Gaps 0;
Qy 3 SGGILLLLGLITLMEVLTVPVSSKDRPDPFCLELPADTGPCRVRFPSFYNNPDEKCLEPIYG 62
Db 10 SRAFLALLSGSLISGLVLAADRSIHDPCLVSKVGRCRASMPRWYNTVDGSCQLFVYG 69
Qy 63 GCEGANNNFTKEKCESTCA 82
Db 70 GCDGNNNNYLTKEKCLKCA 89
Search completed: January 23, 2004, 10:25:15
Job time : 8.59859 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 31.2711 Seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179A-16

Sequence score: 457
1 MSSGGILLILGLTWELVLT.....CEGNANPFYKESCESTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_proteic:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirs:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	457	100.0	83	13	Q90WA1
2	438	95.8	83	13	Q90WA0
3	361	79.0	83	13	Q90W99
4	357	78.1	83	13	Q90W98
5	357	78.1	83	13	Q90W96
6	342	74.8	83	13	Q90W97
7	293	64.1	88	13	Q8AY43
8	287	62.8	88	13	Q8AY41
9	277	60.6	88	13	Q8AY42
10	248	54.3	90	13	Q8AY44
11	241	52.7	90	13	Q8AY45
12	239	52.3	79	13	Q91351
13	201	44.0	90	13	Q8AY46
14	198	43.3	58	5	Q9TWP9
15	194	42.5	85	13	Q9PTA4
16	190	41.6	59	5	Q9TWP8

17	190	41.6	85	13	Q9W728	Q9W728 bungarus mu
18	187.5	41.0	76	5	Q8T7L9	Q8T7L9 bombyx mori
19	187.5	41.0	230	11	Q8CF99	Q8CF99 rattus norv
20	185	40.5	58	5	Q9TWG0	Q9TWG0 anemonia su
21	185	40.5	86	5	Q9GPI5	Q9GPI5 ixodes ricci
22	184.5	40.4	80	5	Q8T357	Q8T357 araneus ven
23	181	39.6	984	5	Q9GQNZ	Q9GQNZ callactis
24	181	39.6	994	5	Q9GQNI	Q9GQNI callactis
25	179	39.2	142	5	Q8WP12	Q8WP12 boophilus m
26	176.5	38.6	142	5	Q8WP13	Q8WP13 boophilus m
27	173	37.9	113	5	Q9V508	Q9V508 drosophila
28	172	37.6	759	5	Q8T191	Q8T191 ancylostoma
29	171.5	37.4	57	5	Q8MTR6	Q8MTR6 haematobia
30	171	37.4	235	11	Q8C180	Q8C180 mus musculu
31	171	37.4	235	11	Q8SB7	Q8SB7 mus musculu
32	169	37.0	396	6	Q28874	Q28874 canis famli
33	167.5	36.7	82	5	Q8MYB4	Q8MYB4 ixodes scap
34	165.5	36.2	1572	5	Q44938	Q44938 haemochus
35	164	35.9	132	5	Q9VQT9	Q9VQT9 drosophila
36	163	35.7	195	11	Q9D8Q8	Q9D8Q8 mus musculu
37	161	35.2	548	4	Q96NZ8	Q96NZ8 homo sapien
38	161	35.2	576	4	Q8TEU8	Q8TEU8 homo sapien
39	161	35.2	3198	5	Q9UGG8	Q9UGG8 manduca sex
40	160.5	35.1	224	4	Q8NAX6	Q8NAX6 homo sapien
41	160	35.0	979	4	Q8N4Z1	Q8N4Z1 homo sapien
42	159	34.8	85	5	Q8WP15	Q8WP15 bombyx mori
43	158	34.6	76	5	Q968S8	Q968S8 galliera me
44	158	34.6	169	6	Q9NOX7	Q9NOX7 bos taurus
45	158	34.6	461	5	Q95822	Q95822 drosophila

ALIGNMENTS

RESULT 1

ID	Q90WA1	PRELIMINARY	PRT	83 AA.
AC	Q90WA1			
DT	01-DEC-2001	(TREMBlrel. 19, Created)		
DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)		
DT	01-MAR-2003	(TREMBlrel. 23, Last annotation update)		
DE	textilis.			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Rhaphidia; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Macci P.P., Layvin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;			
RT	"Plasma inhibitors from the Australian brown snake Pseudonaja			
RT	textilis textilis.";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Filipovich I.V., Sorokina N.I., Macci P.P., de Jersey J.,			
RA	Whitaker A.N., Gaffney P.J., Layvin M.F.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF402324; AAK95519.1; -			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	Prodom; PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KUT; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Protease inhibitor; Serine protease inhibitor.			
SQ	SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;			

Query Match 100.0%; Score 457; DB 13; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCPLPADTGPCVRPSPFYNNPDEKCKLEFI 60
DB 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCPLPADTGPCVRPSPFYNNPDEKCKLEFI 60
OY 61 YGCGEGNANNPTKECESTCA 83
DB 61 YGCGEGNANNPTKECESTCA 83

RESULT 2
O90W90 PRELIMINARY; PRT; 83 AA.
AC O90W90;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Textilinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acantophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402325; AAK95520.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR ProDom; PD000222; Kunitz_BPTI.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9179 MW; 67859AD27175930 CRC64;

Query Match 95.8%; Score 438; DB 13; Length 83;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 79; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402326; AAK95521.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR ProDom; PD000222; Kunitz_BPTI.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9158 MW; 368E82487ACFB61 CRC64;

Query Match 79.0%; Score 361; DB 13; Length 83;
Best Local Similarity 77.1%; Pred. No. 2e-37;
Matches 64; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCPLPADTGPCVRPSPFYNNPDEKCKLEFI 60
DB 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCPLPADTGPCVRPSPFYNNPDEKCKLEFI 60
OY 61 YGCGEGNANNPTKECESTCA 83
DB 61 YGCGEGNANNPTKECESTCA 83

RESULT 4
O90W98 PRELIMINARY; PRT; 83 AA.
AC O90W98;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Textilinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acantophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402327; AAK95522.1;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR ProDom; PD000222; Kunitz_BPTI.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 8983 MW; 3F28548146848A9B CRC64;

Query Match 78.1%; Score 357; DB 13; Length 83;
Best Local Similarity 79.5%; Pred. No. 6.2e-37;
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Matches 66; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 5

ID Q90W96 PRELIMINARY; PRT; 83 AA.
 AC Q90W96;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillinin.
 OS Pseudonaja textilis textilis.
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Maciel P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina I.N., Maciel P.P., de Jersey J.,
 RL Whitaker A.N., Gaffney P.J., Lavlin M.F.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402329; AAK95348.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.1.
 DR PRINTS; PR00759; BASICPTASB.
 DR ProDom; PD000222; Kunitz_BPTI.1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9060 MW; A60DF2692864C58E CRC64;

Query Match 78.1%; Score 357; DB 13; Length 83;
 Best Local Similarity 79.5%; Pred. No. 6.2e-37;
 Matches 66; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 6

ID Q90W97 PRELIMINARY; PRT; 83 AA.
 AC Q90W97;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillinin.
 OS Pseudonaja textilis textilis.
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.

QX NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Maciel P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina I.N., Maciel P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavlin M.F.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402328; AAK95523.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.1.
 DR ProDom; PD000222; Kunitz_BPTI.1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;

Query Match 74.8%; Score 342; DB 13; Length 83;
 Best Local Similarity 77.1%; Pred. No. 4.7e-35;
 Matches 64; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 7

ID Q8AY43 PRELIMINARY; PRT; 88 AA.
 AC Q8AY43;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Kunitz inhibitor a (Fragment).
 OS Bungarus candidus (Malayan Krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.,
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057886; AAL30068.1;
 FT NON TER
 SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 64.1%; Score 293; DB 13; Length 88;
 Best Local Similarity 65.9%; Pred. No. 6.7e-29;
 Matches 54; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 60
 DB 6 MSSGGLLLLGLTLTMEVLTVPVSSKDRPDPFCGLPADTGPCVRPPSFYNDKKCLEFI 65

QY 61 YGCGGANNPITKECESTCA 82
 DB 66 YGCGGANNPITKECESTCA 87

RESULT 8

OBAY41 PRELIMINARY: PRT; 88 AA.
AC OBAY41;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kunitz inhibitor c (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057888; AAL30070.1; --
FT NON TER 1
SQ SEQUENCE 88 AA; 9659 MW; 0279950755FEB787 CRC64;
Query Match 62.8%; Score 287; DB 13; Length 88;
Best Local Similarity 67.1%; Pred. No. 3.8e-28;
Matches 55; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKECESTC 82
DB 66 YGCGGNANPFTKECESTC 87

RESULT 9

OBAY42 PRELIMINARY: PRT; 88 AA.
AC OBAY42;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kunitz inhibitor b (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057887; AAL30069.1; --
FT NON TER 1
SQ SEQUENCE 88 AA; 9391 MW; 71F9P57D36E7A652 CRC64;
Query Match 60.6%; Score 277; DB 13; Length 88;
Best Local Similarity 63.0%; Pred. No. 6.7e-27;
Matches 51; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKECESTC 81
DB 66 YGCGGNANPFTKECESTC 86

RESULT 10

OBAY44 PRELIMINARY: PRT; 90 AA.
AC OBAY44;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungarotoxin B2b chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057885; AAL30067.1; --
FT NON TER 1
SQ SEQUENCE 90 AA; 10281 MW; 15754C179BDE190B CRC64;

Query Match 54.3%; Score 248; DB 13; Length 90;
Best Local Similarity 56.8%; Pred. No. 2.9e-23;
Matches 46; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKECESTC 81
DB 66 YGCGGNANPFTKECESTC 86

RESULT 11

OBAY45 PRELIMINARY: PRT; 90 AA.
AC OBAY45;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungarotoxin B2a chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057884; AAL30066.1; --
FT NON TER 1
SQ SEQUENCE 90 AA; 10122 MW; AD0FBE279D68A910 CRC64;

Query Match 52.7%; Score 241; DB 13; Length 90;
Best Local Similarity 55.6%; Pred. No. 2.2e-22;
Matches 45; Conservative 9; Mismatches 27; Indels 0; Gaps 0;

QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVLTTPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKECESTC 81
DB 66 YGCGGNANPFTKECESTC 86

RESULT 12

091351


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ID 091351 PRELIMINARY; PRT; 79 AA.
AC 091351;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Dendrotoxin K (Fragment).
GN DENDROTOXIN K, DTXK.
OS Dendroaspis polylepis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OC NCBI_TaxId=8624;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277850; PubMed=8504088;
RA Smith L.A., Lafaye P.J., Lapenthiere H.F., Spain T., Dolly J.O.;
RT "Cloning and functional expression of dendrotoxin K from black mamba,
a K+ channel blocker.";
RL Biochemistry 32:5692-5697(1993).
DR EMBL; S61886; AAB26998.1; -.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 79 AA; 8851 MW; DCDP89AFA07D7D46 CRC64;

Query Match 52.3%; Score 239; DB 13; Length 79;
Best Local Similarity 59.5%; Pred. No. 3.4e-22;
Matches 47; Conservative 6; Mismatches 24; Indels 2; Gaps 1;

QY 3 SGGILLILGLTLTWBLTPVSSKDRDPCELPADTGPCRVRFPSPFYNDPEKKCLEFIYG 62
DB 1 SGGILLILGLTLTWBLTPVSSGAK--YCKLPLRIGPCRKIPSPFYKKAKQCLPFDVS 58

QY 63 GCGGNANPITKECESTC 81
DB 59 GCGGNANPITKECESTC 77

RESULT 13
ID 08AY46 PRELIMINARY; PRT; 90 AA.
AC 08AY46;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Beta bungarotoxin BI chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxId=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBD databases.
DR EMBL; AY057883; AAL30065.1; -.
SQ SEQUENCE 90 AA; 10048 MW; E05C2A0D28179726 CRC64;

Query Match 44.0%; Score 201; DB 13; Length 90;
Best Local Similarity 53.1%; Pred. No. 2.2e-17;
Matches 43; Conservative 6; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSSGILLILGLTLTWBLTPVSSKDRDPCELPADTGPCRVRFPSPFYNDPEKKCLEFI 60

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DB 6 MSSGILLILGLTLTWBLTPVSSRQRHDCDPPDKNGSVYRAFYDTRLTCKAFP 65
QY 61 YGCGGNANPITKECESTC 81
DB 66 YGCGGNANPITKECESTC 86

RESULT 14
ID 09TFP9 PRELIMINARY; PRT; 58 AA.
AC 09TFP9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE KALITUDINE 2, ASK2.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;
OC NCB1_TaxId=6108;
RN [1]
RP SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guilleme E., Moliner D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicludines and kalipeptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSSP; P12111; ZKNT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; P102E71682P1A55C CRC64;

Query Match 43.3%; Score 198; DB 5; Length 58;
Best Local Similarity 62.7%; Pred. No. 3.3e-17;
Matches 32; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 31 CELPADTGPCRVRFPSPFYNDPEKKCLEFIYGCCEGNANPITKECESTC 81
DB 5 CELPADTGPCRVRFPSPFYNDPEKKCLEFIYGCCEGNANPITKECESTC 55

RESULT 15
ID 09PTA4 PRELIMINARY; PRT; 85 AA.
AC 09PTA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Beta-bungarotoxin BI precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxId=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wu P.F., Chang L.S.;
RT "Genetic structures of A chain and B chain of beta-bungarotoxin from
RT Taiwan Banded krait (Bungarus multicinctus). A chain genes and B chain
RT genes do not share a common origin.";
RL Eur. J. Biochem. 267:4668-4675(2000).
DR EMBL; AJ251223; CAB62503.1; -.
DR HSSP; P00981; IDTK.

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DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor; signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 1 85 BETA-BUNGAROTOXIN B1.
 SQ SEQUENCE 85 AA; 9555 MW; BSA78452AE7CC55C CRC64;

Query Match. 42.5%; Score 194; DB 13; Length 85;
 Best Local Similarity 51.9%; Pred. No. 1.6e-16;
 Matches 42; Conservative 6; Mismatches 33; Indels 0; Gaps 0;

QY	1	MSSGGLLLGLTLTMEVLTVPVSSKDRPDPCELPADTPGCRVRFPSFTYNDEKCLEFI	60
DB	1	MSSGGLLLGLTLTSAELIPVSSQRHRDCDKPPKNGCGPVRRAFYYDTRLKTKCAFQ	60
QY	61	YGCCEGNANNPITKECESTC	81
DB	61	YRGCGNGNHRKTETLCRCRC	81

Search completed: January 23, 2004, 10:27:16
 Job time : 31.2711 secs

A:Reference number: A44180; MUID:93134601; PMID:1485334

A:Accession: A44180

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-62 <POS>

A:Experimental source: subsp. scutellatus, venom

A>Note: sequence extracted from NCBI backbone (NCBI:P122482)

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.5%; Score 217; DB 2; Length 62;

Best Local Similarity 63.2%; Pred. No. 1.6e-16;

Matches 36; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 81

Db 1 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 57

RESULT 3

TIIVIC

venom basic proteinase inhibitor III - sand viper

N:Alternate names: venom chymotrypsin inhibitor

C:Species: Viper aamodytes (sand viper)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #ext_change 16-Aug-1996

C:Accession: A01223

R:Ritonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 138-145, 1983

A:Title: The primary structure Of Viper aamodytes venom chymotrypsin inhibitor.

A:Reference number: A01223

A:Molecule type: protein

A:Residues: 1-65 <RT>

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Diulfide bonds: #status predicted

F:17/inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 46.8%; Score 214; DB 1; Length 65;

Best Local Similarity 62.7%; Pred. No. 3.5e-16;

Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 83

Db 1 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 59

RESULT 4

S07451

proteinase inhibitor 5.II - snake-locks sea anemone

C:Species: Anemonea sulcata (snake-locks sea anemone)

C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #ext_change 09-May-1997

C:Accession: S07451; B27222

R:Munderer, G.; Machleidt, W.; Fritze, H.

Meth. Enzymol. 80, 816-820, 1981

A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonea

A:Reference number: S07451

A:Molecule type: protein

A:Residues: 1-59 <WUN>

A>Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R:Krebs, H.C.; Habermann, G.G.

Naturwissenschaften 74, 395-396, 1987

A:Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der

A:Reference number: A94700

A:Molecule type: protein

A:Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'ZZ', '51', 'Z', '53-62 <KRB>

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor

F:5-55/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 44.6%; Score 204; DB 2; Length 62;

Best Local Similarity 66.7%; Pred. No. 4e-15;

Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 31 CELPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 81

Db 5 CELPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 55

RESULT 5

TIIVIC

venom basic proteinase inhibitor II - Cape cobra

C:Species: Naja naja (Cape cobra)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #ext_change 16-Aug-1996

C:Accession: A01217

R:Hoekema, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.

J. Biochem. 79, 559-578, 1976

A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibi

o acid sequences of two of them.

A:Reference number: A01217; MUID:76237547; PMID:950337

A:Molecule type: protein

A:Residues: 1-57 <HOK>

C:Comment: The activity of this inhibitor is probably similar to that of bovine basic

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor hom

C:Keywords: serine proteinase inhibitor; venom

F:5-55/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:5-55,14-38,30-51/Diulfide bonds: #status predicted

Query Match 44.0%; Score 201; DB 1; Length 57;

Best Local Similarity 63.6%; Pred. No. 7.6e-15;

Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 27 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 81

Db 1 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 55

RESULT 6

TIIVIC

venom basic proteinase inhibitor I - western sand viper

N:Alternate names: venom trypsin inhibitor I

C:Species: Viper aamodytes amodytes (western sand viper)

C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #ext_change 16-Aug-1996

C:Accession: A01222

R:Ritonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 429-435, 1983

A:Title: The primary structure of Viper aamodytes venom trypsin inhibitor I.

A:Reference number: A01222; MUID:84053385; PMID:6639951

A:Molecule type: protein

A:Residues: 1-61 <RT>

C:Comment: This protein inhibits trypsin and kallikrein.

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor hom

C:Keywords: pyroglutamic acid; serine proteinase inhibitor; venom

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Diulfide bonds: #status predicted

F:17/inhibitory site: Lys (trypsin) #status predicted

Query Match 44.0%; Score 201; DB 1; Length 61;

Best Local Similarity 57.6%; Pred. No. 8.2e-15;

Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 83

Db 1 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLFYGGCGGNANFTTKECSESTC 59

RESULT 7

TIIVIC

venom basic proteinase inhibitor II - ringhals

C/Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C/Accession: A01216
R/Sokana, Y.; Iwanaga, S.; Tateuchi, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A/Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
o acid sequences of two of them.
A/Reference number: A91942; MUID:76237547; PMID:950337
A/Accession: A01216
A/Molecule type: protein
A/Residues: 1-57 <HOK>
C/Comment: The activity of this inhibitor is similar to that of bovine basic protease in
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom
F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/5-55,14-38,30-51/Dissulfide bonds: #status predicted

Query Match 43.3%; Score 198; DB 1; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.66-14;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 81
DB 1 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 55

RESULT 8

S19327

venom basic proteinase inhibitor - leaf-nosed viper

N/Alternate names: trypsin inhibitor (Kunitz-type)

C/Species: Eristocophis machaboni (leaf-nosed viper)

C/Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999

C/Accession: S19327

R/Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.

FEBS Lett. 294, 141-143, 1991

A/Title: Purification and characterization of a Kunitz-type trypsin inhibitor from leaf-

A/Reference number: S19327; MUID:92077130; PMID:1743283

A/Accession: S19327

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-62 <SID>

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F/2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.7%; Score 195; DB 2; Length 62;
Best Local Similarity 61.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTCA 83
DB 1 FCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTCA 54

RESULT 9

S13846

venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)

C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000

C/Accession: S13846

R/Shafiq, J.; Beg, O.U.; Yln, S.J.; Zaidi, Z.H.; Joernvall, H.

Eur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja naja) venom Kunitz-

A/Reference number: S13846; MUID:9109304; PMID:1702708

A/Accession: S13846

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SHA>

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.5%; Score 194; DB 2; Length 57;

Best Local Similarity 60.0%; Pred. No. 4.3e-14;
Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 81
DB 1 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 55

RESULT 10

TITROR

basic proteinase inhibitor - loggerhead

C/Species: Caretta caretta (loggerhead)

C/Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C/Accession: A01224

R/Kato, I.; Tomimaga, N.

Fed. Proc. 38, 832, 1979

A/Title: Trypsin-subtilisin inhibitor from red sea turtle-eggwhite consists of two tr

A/Reference number: A01224

A/Accession: A01224

A/Molecule type: protein

A/Residues: 1-110 <KAT>

C/Comment: This inhibitor, isolated from egg white, consists of two nonhomologous doma

C/Superfamily: logerthead basic proteinase inhibitor; animal Kunitz-type proteinase in

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F/8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/63-105/Domain: antileukoproteinase repeat homology <ALP>

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8-58,17-41,33-54,67-93,76-97,80-92,86-101/Dissulfide bonds: #status predicted

F/18/Inhibitory site: Lys (trypsin) #status predicted

Query Match 41.4%; Score 189; DB 1; Length 110;
Best Local Similarity 53.6%; Pred. No. 2.9e-13;
Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 26 DRPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 81
DB 3 DRPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 58

RESULT 11

TIRHAK

isoInhibitor K (BPI type) - Roman snail

C/Species: Helix pomatia (Roman snail)

C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C/Accession: A91232; A01225

R/Teschke, H.; Dietl, T.

Eur. J. Biochem. 58, 439-451, 1975

A/Title: The amino-acid sequence of isoInhibitor K from snails (Helix pomatia). A sequ

A/Reference number: A91232; MUID:76043680; PMID:1183446

A/Accession: A91232

A/Molecule type: protein

A/Residues: 1-58 <TSC>

R/Dietl, T.; Teschke, H.

Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976

A/Title: Die Disulfidbrücken des Trypsin-Kallikrein-Inhibitoren K aus Weinbergaschnecker

A/Reference number: A91665; MUID:76141310; PMID:3462

A/Contents: annotation; disulfide bonds

C/Comment: This is one of several isoInhibitors of broad specificity that are secreted

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/7-57,16-40,32-53/Dissulfide bonds: #status predicted

Query Match 41.1%; Score 188; DB 1; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.9e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 81
DB 3 RPDCELPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFRTKECESTC 57

RESULT 12

B59399

short epsilon-dendrotoxin H1a55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C:Accession: B59399

R:Single, R.: Hackett, M.; Aird, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: B59399

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-57 <AIR>

A:Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F:5-55/Disulfide bonds: #status experimental

F:14-38/Disulfide bonds: #status experimental

F:30-51/Disulfide bonds: #status experimental

Query Match 39.2%; Score 179; DB 2; Length 57;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSPFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81

Db 4 FCKLPABPGPCKASIPAFYNNMAKKCOLFHYGCKGNANRSTIEKCRHAC 55

RESULT 13

TIPEPD

venom basic proteinase inhibitor E - black mamba

C:Species: Dendroaspis polyolepis polyolepis (black mamba)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01215

R:Joubert, F.J.; Stolydom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A:Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis pol

A:Reference number: A01215; MUID:78214615; PMID:668688

A:Accession: A01215

A:Molecule type: protein

A:Residues: 1-59 <JOU>

A:Note: this protein inhibits trypsin and binds transition metal ions such as copper and

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 39.2%; Score 179; DB 1; Length 59;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSPFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81

Db 6 FCKLPABPGPCKASIPAFYNNMAKKCOLFHYGCKGNANRSTIEKCRHAC 57

RESULT 14

A59399

long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C:Accession: A59399

R:Single, R.: Hackett, M.; Aird, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: A59399

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-59 <AIR>

A:Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F:7-57/Disulfide bonds: #status experimental

F:16-40/Disulfide bonds: #status experimental

F:32-53/Disulfide bonds: #status experimental

Query Match 39.2%; Score 179; DB 2; Length 59;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSPFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81

Db 6 FCKLPABPGPCKASIPAFYNNMAKKCOLFHYGCKGNANRSTIEKCRHAC 57

RESULT 15

TIVRY2

venom basic proteinase inhibitor II - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01221

R:Takahashi, H.; Iwanaga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.

J. Biochem. 76, 721-733, 1974

A:Title: Snake venom proteinase inhibitor. II. Chemical structure of inhibitor II iso

A:Reference number: A01221; MUID:75060360; PMID:4436285

A:Accession: A01221

A:Molecule type: protein

A:Residues: 1-60 <TAK>

C:Comment: This inhibitor has activity similar to that of bovine basic protease inhibi

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 38.9%; Score 178; DB 1; Length 60;

Best Local Similarity 53.6%; Pred. No. 2.4e-12;

Matches 30; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 26 DRPFCCLPADTGPCRVPRPSPFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81

Db 2 DRPFCCLPADTGPCRVPRPSPFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 57

Search completed: January 23, 2004, 10:28:11
Job time : 13.8592 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:27:24 ; Search time 29.8099 Seconds
(without alignments)
575.620 Million cell updates/sec

Title: US-09-700-179a-16

Perfect score: 457
Sequence: 1 MSSGGILLGLITLMEVLT.....CEGNANFTKECESTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	221	48.4	58	12	US-10-038-722-5
2	214	46.8	62	12	US-10-038-722-110
3	214	46.8	62	12	US-09-896-095-167
4	204	44.6	59	12	US-10-038-722-112
5	204	44.6	59	12	US-09-896-095-169
6	202	44.2	58	12	US-10-167-351-69
7	201	44.0	57	12	US-10-038-722-101
8	201	44.0	57	12	US-09-896-095-158
9	201	44.0	58	12	US-10-167-351-65
10	201	44.0	61	12	US-10-038-722-109
11	201	44.0	61	12	US-09-896-095-166
12	198	43.3	57	12	US-10-038-722-100
13	198	43.3	57	12	US-09-896-095-157
14	192	42.0	58	12	US-10-167-351-75
15	192	42.0	62	12	US-10-038-722-111

16	192	42.0	62	12	US-09-896-095-168	Sequence 168, App
17	189	41.4	58	12	US-10-167-351-67	Sequence 67, App
18	189	41.4	64	12	US-10-038-722-103	Sequence 103, App
19	189	41.4	64	12	US-09-896-095-160	Sequence 160, App
20	186	40.7	58	12	US-10-167-351-71	Sequence 71, App
21	186	40.7	60	12	US-10-038-722-102	Sequence 102, App
22	186	40.7	60	12	US-09-896-095-159	Sequence 159, App
23	185	40.5	86	10	US-09-910-430-8	Sequence 8, App
24	185	40.5	86	15	US-10-165-605A-8	Sequence 8, App
25	184	40.3	58	12	US-10-038-722-55	Sequence 55, App
26	182	39.8	58	12	US-10-038-722-17	Sequence 17, App
27	182	39.8	58	12	US-10-038-722-41	Sequence 41, App
28	182	39.8	58	12	US-10-038-722-104	Sequence 104, App
29	182	39.8	58	12	US-09-896-095-161	Sequence 161, App
30	181	39.6	57	12	US-10-038-722-105	Sequence 105, App
31	181	39.6	57	12	US-09-896-095-162	Sequence 162, App
32	181	39.6	58	12	US-10-038-722-18	Sequence 18, App
33	181	39.6	58	12	US-10-038-722-19	Sequence 19, App
34	180	39.4	58	12	US-10-038-722-43	Sequence 43, App
35	180	39.4	58	12	US-10-038-722-49	Sequence 49, App
36	180	39.4	240	12	US-09-974-026-47	Sequence 47, App
37	180	39.4	252	9	US-09-827-948-2	Sequence 2, App
38	180	39.4	252	12	US-10-176-071-2	Sequence 2, App
39	180	39.4	252	12	US-09-974-026-49	Sequence 49, App
40	180	39.4	252	15	US-10-097-340-302	Sequence 302, App
41	180	39.4	270	12	US-10-264-049-3083	Sequence 3083, App
42	180	39.4	289	9	US-09-925-301-1266	Sequence 1266, App
43	179	39.2	58	12	US-10-167-351-62	Sequence 62, App
44	179	39.2	59	12	US-10-038-722-108	Sequence 108, App
45	179	39.2	59	12	US-09-896-095-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-038-722-5
Sequence 5, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/649,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5
Query Match 48.4%; Score 221; DB 12; Length 58;
Best Local Similarity 69.1%; Pred. No. 3.5e-18;
Matches 38; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
27 RDPCFLPADTGPCRVRRPSPFYNDPEKKLEBIEYGCCEGNANFTKECESTC 81
1 RDPCFLPADTGPCRVRRPSPFYNDPEKKLEBIEYGCCEGNANFTKECESTC 55

RESULT 2

US-10-038-722-110

; Sequence 110, Application US/10038722

; Publication No. US20030175919A1

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: MARKLAND, William

; APPLICANT: KENT, Rachel B.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: LADNER, Robert C.

; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS

; FILE REFERENCE: LEY-1B

; CURRENT APPLICATION NUMBER: US/10/038,722

; CURRENT FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 08/849,406

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: PCT/US95/16349

; PRIOR FILING DATE: 1995-12-15

; PRIOR APPLICATION NUMBER: US 08/358,160

; PRIOR FILING DATE: 1994-12-16

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 110

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Vipera ammodytes

US-10-038-722-110

Query Match 46.8%; Score 214; DB 12; Length 62;

Best Local Similarity 62.7%; Pred. No. 2.4e-17;

Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPDPCELPADTGPCRVPRFPSPFYNDPEKCKLEFIYGGCGGNANNTKECESTCA 83

Db 1 RDRPKFCYLPADTGPCRLAIVPRFYNDPASNKCKEFTIYGGCGGNANNTKEDCHTCA 59

RESULT 3

US-09-896-095-167

; Sequence 167, Application US/09896095

; Publication No. US20030219886A1

; GENERAL INFORMATION:

; APPLICANT: LADNER, Charles C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: MARKLAND, William

; APPLICANT: LEY, Arthur C.

; APPLICANT: KENT, Rachel B.

; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS

; FILE REFERENCE: LADNER-7L

; CURRENT APPLICATION NUMBER: US/09/896,095

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 08/415,922

; PRIOR FILING DATE: 1995-03-04

; PRIOR APPLICATION NUMBER: 08/009,319

; PRIOR FILING DATE: 1993-01-26

; PRIOR APPLICATION NUMBER: 07/664,989

; PRIOR FILING DATE: 1991-03-01

; PRIOR APPLICATION NUMBER: 08/993,776

; PRIOR FILING DATE: 1997-12-18

; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 167

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Vipera ammodytes

US-09-896-095-167

Query Match 46.8%; Score 214; DB 12; Length 62;

Best Local Similarity 62.7%; Pred. No. 2.4e-17;

Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPDPCELPADTGPCRVPRFPSPFYNDPEKCKLEFIYGGCGGNANNTKECESTCA 83

Db 1 RDRPKFCYLPADTGPCRLAIVPRFYNDPASNKCKEFTIYGGCGGNANNTKEDCHTCA 59

RESULT 4

US-10-038-722-112

; Sequence 112, Application US/10038722

; Publication No. US20030175919A1

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: MARKLAND, William

; APPLICANT: KENT, Rachel B.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: LADNER, Robert C.

; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS

; FILE REFERENCE: LEY-1B

; CURRENT APPLICATION NUMBER: US/10/038,722

; CURRENT FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 08/849,406

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: PCT/US95/16349

; PRIOR FILING DATE: 1995-12-15

; PRIOR APPLICATION NUMBER: US 08/358,160

; PRIOR FILING DATE: 1994-12-16

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 112

; LENGTH: 59

; TYPE: PRT

; ORGANISM: Anemomia sulcata

US-10-038-722-112

Query Match 44.6%; Score 204; DB 12; Length 59;

Best Local Similarity 66.7%; Pred. No. 3.3e-16;

Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 31 CEIPADTGPCRVPRFPSPFYNDPEKCKLEFIYGGCGGNANNTKECESTC 81

Db 5 CEIPKVVGPCRVPRFPFYNDPSSKCKEFTIYGGCGGNANNTKECESTC 55

RESULT 5

US-09-896-095-169

; Sequence 169, Application US/09896095

; Publication No. US20030219886A1

; GENERAL INFORMATION:

; APPLICANT: LADNER, Charles C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: MARKLAND, William

; APPLICANT: LEY, Arthur C.

; APPLICANT: KENT, Rachel B.

; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS

; FILE REFERENCE: LADNER-7L

; CURRENT APPLICATION NUMBER: US/09/896,095

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 08/415,922

; PRIOR FILING DATE: 1995-03-04

; PRIOR APPLICATION NUMBER: 08/009,319

; PRIOR FILING DATE: 1993-01-26

; PRIOR APPLICATION NUMBER: 07/664,989

; PRIOR FILING DATE: 1991-03-01

; PRIOR APPLICATION NUMBER: 08/993,776

; PRIOR FILING DATE: 1997-12-18

; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 169

; LENGTH: 59

; TYPE: PRT

; ORGANISM: Vipera ammodytes

US-09-896-095-169

ORGANISM: Anemonia sulcata
US-09-896-095-169

Query Match 44.6%; Score 204; DB 12; Length 59;
Best Local Similarity 66.7%; Pred. No. 3.3e-16;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 31 CELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 81
DB 5 CELPVGECRAFPRIYNNSSKCKEFTIYGGCGGNANNFITKECEKVC 55

RESULT 6
US-10-167-351-69

Sequence 69, Application US/10167351
Publication No. US20030165896A1

GENERAL INFORMATION:

APPLICANT: DYAX CORP.

APPLICANT: Markland, William

APPLICANT: Lader, Robert C.

TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains

FILE REFERENCE: DYX-007.2P US-4

CURRENT FILING DATE: 2002-06-11

PRIOR APPLICATION NUMBER: 09/638,770

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 09/414,878

PRIOR FILING DATE: 1999-10-08

PRIOR APPLICATION NUMBER: 09/240,136

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 08/676,124

PRIOR FILING DATE: 1997-01-07

PRIOR APPLICATION NUMBER: PCT/US95/00298

PRIOR FILING DATE: 1995-01-11

PRIOR APPLICATION NUMBER: 08/208,265

PRIOR FILING DATE: 1994-03-10

PRIOR APPLICATION NUMBER: 08/179,658

PRIOR FILING DATE: 1994-01-11

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patent in version 3.1

SEQ ID NO 69

LENGTH: 58

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: designed plasmin inhibitor

US-10-167-351-69

Query Match 44.2%; Score 202; DB 12; Length 58;
Best Local Similarity 59.3%; Pred. No. 5.5e-16;

Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 29 DPCFELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 82
DB 3 DICKLPKDTGPRARPRDKWYDNTSKCEFFYGGCGGNENKSGSKCEKVC 56

RESULT 7
US-10-038-722-101

Sequence 101, Application US/10038722
Publication No. US20030175919A1

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: LADNER, Robert C.

TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS

FILE REFERENCE: LEY-1B

CURRENT APPLICATION NUMBER: US/10/038,722

CURRENT FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 08/849,406

PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349

PRIOR FILING DATE: 1995-12-15

PRIOR APPLICATION NUMBER: US 08/358,160

PRIOR FILING DATE: 1994-12-16

NUMBER OF SEQ ID NOS: 129

SOFTWARE: Patent in version 3.1

SEQ ID NO 101

LENGTH: 57

TYPE: PRT

ORGANISM: Naia nivea

US-10-038-722-101

Query Match 44.0%; Score 201; DB 12; Length 57;
Best Local Similarity 63.6%; Pred. No. 7.1e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 27 RDPFCELPAITGTCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 81
DB 1 RRFCELPAITGTCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 55

RESULT 8
US-09-896-095-158

Sequence 158, Application US/09896095
Publication No. US20030219886A1

GENERAL INFORMATION:

APPLICANT: LADNER, Charles C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARKLAND, William

APPLICANT: LEY, Arthur C.

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS

FILE REFERENCE: LADNER-7L

CURRENT APPLICATION NUMBER: US/09/896,095

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 08/415,922

PRIOR FILING DATE: 1995-03-04

PRIOR APPLICATION NUMBER: 08/009,319

PRIOR FILING DATE: 1993-01-26

PRIOR APPLICATION NUMBER: 07/664,989

PRIOR FILING DATE: 1991-03-01

PRIOR APPLICATION NUMBER: 08/393,776

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 274

SOFTWARE: Patent in version 3.2

SEQ ID NO 158

LENGTH: 57

TYPE: PRT

ORGANISM: Naia nivea

US-09-896-095-158

Query Match 44.0%; Score 201; DB 12; Length 57;
Best Local Similarity 63.6%; Pred. No. 7.1e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 27 RDPFCELPAITGTCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 81
DB 1 RRFCELPAITGTCRVPRPSFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 55

RESULT 9
US-10-167-351-65

Sequence 65, Application US/10167351
Publication No. US20030165896A1

GENERAL INFORMATION:

APPLICANT: DYAX CORP.

APPLICANT: Markland, William

APPLICANT: Lader, Robert C.

TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains

FILE REFERENCE: DYX-007.2P US-4

CURRENT APPLICATION NUMBER: US/10/167,351

```

; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 65
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: designed plasmin inhibitor
US-10-167-351-65
```

```

Query Match      44.0%; Score 201; DB 12; Length 58;
Best Local Similarity 61.8%; Pred. No. 7.2e-16;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
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Qy      27 RPDPCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTC 81
Db      1 KDPFCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTC 55
```

```

RESULT 10
US-10-038-722-109
; Sequence 109, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 109
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-10-038-722-109
```

```

Query Match      44.0%; Score 201; DB 12; Length 61;
Best Local Similarity 57.6%; Pred. No. 7.6e-16;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
```

```

Qy      25 KDRPFCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 83
Db      1 ZDHPFCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 59
```

RESULT 11

```

US-09-896-095-166
; Sequence 166, Application US/09896095
; Publication No. US20030219866A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-71
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 166
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-896-095-166
```

```

Query Match      44.0%; Score 201; DB 12; Length 61;
Best Local Similarity 57.6%; Pred. No. 7.6e-16;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
```

```

Qy      25 KDRPFCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 83
Db      1 ZDHPFCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 59
```

```

RESULT 12
US-10-038-722-100
; Sequence 100, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 100
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Hemachatus hemachatus
US-10-038-722-100
```

```

Query Match      43.3%; Score 198; DB 12; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.6e-15;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
```

```

Qy      27 RPDPCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTC 81
```

Db 1 RDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 55

RESULT 13
US-09-896-095-157

Sequence 157, Application US/09896095
Publication No. US20030219886A1
GENERAL INFORMATION:
APPLICANT: LADNER, Charles C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: LEY, Arthur C.
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
FILE REFERENCE: LADNER=7L
CURRENT APPLICATION NUMBER: US/09/896,095
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 08/415,922
PRIOR FILING DATE: 1995-03-04
PRIOR APPLICATION NUMBER: 08/009,319
PRIOR FILING DATE: 1993-01-26
PRIOR APPLICATION NUMBER: 07/664,989
PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 08/993,776
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn version 3.2
SEQ ID NO 157
LENGTH: 57
TYPE: PRT
ORGANISM: Hemachatus hemachates
US-09-896-095-157

Query Match 43.3%; Score 198; DB 12; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.6e-15;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 27 RDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 81
Db 1 RDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 55

RESULT 14
US-10-167-351-75

Sequence 75, Application US/10167351
Publication No. US20030165896A1
GENERAL INFORMATION:
APPLICANT: DYAX CORP.
APPLICANT: Markland, William
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
FILE REFERENCE: DYX-007.2P US-4
CURRENT APPLICATION NUMBER: US/10/167,351
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/638,770
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/414,878
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/240,136
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 08/676,124
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: PCT/US95/00298
PRIOR FILING DATE: 1995-01-11
PRIOR APPLICATION NUMBER: 08/208,265
PRIOR FILING DATE: 1994-03-10
PRIOR APPLICATION NUMBER: 08/179,658
PRIOR FILING DATE: 1994-01-11
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75

LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: designed plasmin inhibitor
US-10-167-351-75

Query Match 42.0%; Score 192; DB 12; Length 58;
Best Local Similarity 54.5%; Pred. No. 7.9e-15;
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 28 PDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 82
Db 2 PDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 56

RESULT 15
US-10-038-722-111

Sequence 111, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY=1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 111
LENGTH: 62
TYPE: PRT
ORGANISM: Bungarus fasciatus
US-10-038-722-111

Query Match 42.0%; Score 192; DB 12; Length 62;
Best Local Similarity 57.6%; Pred. No. 8.5e-15;
Matches 34; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 25 KDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 83
Db 1 KDPFCELPAETGICXAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 59

Search completed: January 23, 2004, 10:43:29
Job time : 29.8099 sec

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OM protein - protein search, using SW model

Run on: January 23, 2004, 10:22:13 (Search time 13.7359 Seconds
(without alignments)
255.666 Million cell updates/sec

Title: US-09-700-179a-16
Sequence score: 457
Sequence: 1 MESSGILLILGLTWELT.....CEGNANPTKRCESSTCA 83

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgm2_6/prodata/1/1aa/5B COMB.pep.*
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4: /cgm2_6/prodata/1/1aa/6B COMB.pep.*
5: /cgm2_6/prodata/1/1aa/PCITUS COMB.pep.*
6: /cgm2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	221	48.4	58	1	US-08-358-160-71
2	217	47.5	65	6	5466783-12
3	214	46.8	65	1	US-08-358-160-92
4	204	44.6	62	1	US-08-358-160-97
5	202	44.2	58	3	US-08-676-124-69
6	202	44.2	58	3	US-09-414-878-69
7	202	44.2	58	3	US-09-240-136-69
8	202	44.2	58	4	US-09-638-770A-69
9	201	44.0	57	1	US-08-358-160-99
10	201	44.0	58	3	US-08-676-124-65
11	201	44.0	58	3	US-09-414-878-65
12	201	44.0	58	3	US-09-240-136-65
13	201	44.0	58	4	US-09-638-770A-65
14	201	44.0	61	1	US-08-358-160-91
15	198	43.3	57	1	US-08-358-160-94
16	198	43.3	57	6	5466783-9
17	195	42.7	61	1	US-08-358-160-93
18	194	42.5	57	1	US-08-358-160-108
19	192.5	42.1	60	6	5466783-8
20	192	42.0	58	3	US-08-676-124-75
21	192	42.0	58	3	US-09-414-878-75
22	192	42.0	58	3	US-09-240-136-75
23	192	42.0	58	4	US-09-638-770A-75
24	192	42.0	65	1	US-08-358-160-96
25	190.5	41.7	58	6	5466783-10
26	189	41.4	58	3	US-08-676-124-67
27	189	41.4	58	3	US-09-414-878-67

28	189	41.4	58	3	US-09-240-136-67	Sequence 67, Appl
29	189	41.4	58	4	US-09-638-770A-67	Sequence 67, Appl
30	189	41.4	66	1	US-08-358-160-113	Sequence 113, App
31	189	41.4	79	6	5466783-7	Patent No. 5466783
32	188	41.1	58	1	US-08-358-160-116	Sequence 116, App
33	186	40.7	58	3	US-08-676-124-71	Sequence 71, Appl
34	186	40.7	58	3	US-09-414-878-71	Sequence 71, Appl
35	186	40.7	58	3	US-09-240-136-71	Sequence 71, Appl
36	186	40.7	58	4	US-09-638-770A-71	Sequence 71, Appl
37	186	40.7	60	1	US-08-358-160-95	Sequence 95, Appl
38	181	39.6	57	1	US-08-358-160-103	Sequence 103, App
39	181	39.6	58	1	US-08-358-160-17	Sequence 17, Appl
40	181	39.6	58	1	US-08-358-160-18	Sequence 18, Appl
41	180	39.4	58	1	US-08-358-160-12	Sequence 12, Appl
42	180	39.4	240	4	US-09-144-428-47	Sequence 47, Appl
43	180	39.4	252	1	US-08-685-660A-7	Sequence 7, Appl
44	180	39.4	252	2	US-08-974-195-7	Sequence 7, Appl
45	180	39.4	252	3	US-09-071-709-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-358-160-71
Sequence 71, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-71

Query Match 48.4%; Score 221; DB 1; Length 58;
Best Local Similarity 69.1%; Pred. No. 3.1e-20;
Matches 38; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 27 RPDCELPAADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTC 81
Db 1 RPDCELPAADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTC 55

RESULT 2
5466783-12
Patent No. 5466783
APPLICANT: Wu, Tze-Chen, Kretzmer, Kuniko K., Broze,
George J. Jr.
TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/93,285
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,280
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 123,753
FILING DATE: 23-NOV-1987
APPLICATION NUMBER: 77,366
FILING DATE: 23-JUL-1987
SEQ ID NO: 12
LENGTH: 65
5466783-12

Query Match 47.5%; Score 217; DB 6; Length 65;
Best Local Similarity 62.7%; Pred. No. 1.1e-19;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCFLPADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTCA 83
Db 1 RDRPFCTLPADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTCA 59

RESULT 3
US-08-358-160-92
Sequence 92, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-92

Query Match 46.8%; Score 214; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 2.6e-19;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCFLPADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTCA 83
Db 1 RDRPFCTLPADTGCRVRFPSPFYNNPDEKCLEFIYGCCEGANNNTKEBCSTCA 59

RESULT 4
US-08-358-160-97
Sequence 97, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-97

Query Match 44.6%; Score 204; DB 1; Length 62;
Best Local Similarity 66.7%; Pred. No. 4,2e-18;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Db 31 CELPADTGPCRVPRPSFYNNPDEKCLEFTYGGCGGNANPITKECESTC 81
5 CELPKVGPGRARFPRTYNNSSKRCCKFTYGGCGGNANPHTIECEKVC 55

RESULT 5
US-08-676-124-69
Sequence 69, Application US/08676124
Patent No. 6010880
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6,8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Db 29 DFCPLADTGPCRVPRPSFYNNPDEKCLEFTYGGCGGNANPITKECESTCA 82
3 DICKLPDTPGRARFPRTYNNSSKRCCKFTYGGCGGNANPHTIECEKVC 56

RESULT 6
US-09-414-878-69
Sequence 69, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R.
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P.
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6,8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 29 DCELPADTGPCRVRFPSFYNNPDEKCLLFYGGCGEGNANNFTKECESTCA 82
Db 3 DICKLPKDTGCRARFDMKYDDPNTKSCERFYGGCGGNNENKFGSQKECEKCA 56

RESULT 7
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSER: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R.
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P

REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6,8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 29 DCELPADTGPCRVRFPSFYNNPDEKCLLFYGGCGEGNANNFTKECESTCA 82
Db 3 DICKLPKDTGCRARFDMKYDDPNTKSCERFYGGCGGNNENKFGSQKECEKCA 56

RESULT 8
US-09-638-770A-69
Sequence 69, Application US/09638770A
Patent No. 6423498
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 69;
US-09-638-770A-69

Query Match 44.2%; Score 202; DB 4; Length 58;
Best Local Similarity 59.3%; Pred. No. 6.8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 29 DPCELPADTGPCRVPRPSFYNNPDEKCLFEIYGGCGGNANNFITKECESTCA 82
Db 3 DICKLPDTPGCRARFDKMYIDPNTKSCERFYGGCGGNENKFGSGCEKCYCA 56

RESULT 9
US-08-358-160-99
Sequence 99, Application US/08358160

Patent No. 5663143

GENERAL INFORMATION:

APPLICANT: LEV, Arthur C.

APPLICANT: LADNER, Robert C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARLAND, William

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133, 031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009, 319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664, 989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487, 063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240, 160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28, 005

REFERENCE/DOCKET NUMBER: LEV=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 57 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-358-160-99

Query Match 44.0%; Score 201; DB 1; Length 57;
Best Local Similarity 63.6%; Pred. No. 8.9e-18;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RPDFCELPADTGPCRVPRPSFYNNPDEKCLFEIYGGCGGNANNFITKECESTC 81
Db 1 RPRCELPADTGPCRVPRPSFYNNPDEKCLFEIYGGCGGNANNFITKECESTC 55

RESULT 10
US-08-676-124-65
Sequence 65, Application US/08676124

Patent No. 6010880

GENERAL INFORMATION:

APPLICANT: MARLAND, William

APPLICANT: LADNER, Robert Charles

TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED

TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS

NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/676, 124

FILING DATE: 11-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/00238

FILING DATE: 11-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179, 658

FILING DATE: 11-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/208, 265

FILING DATE: 10-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 28, 005

REFERENCE/DOCKET NUMBER: MARLAND=3B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-676-124-65

Query Match 44.0%; Score 201; DB 3; Length 58;
Best Local Similarity 61.8%; Pred. No. 9.1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 27 RPDFCELPADTGPCRVPRPSFYNNPDEKCLFEIYGGCGGNANNFITKECESTC 81
Db 1 KPDRCELPADTGPCRVPRPSFYNNPDEKCLFEIYGGCGGNANNFITKECESTC 55

RESULT 11
US-09-414-878-65
Sequence 65, Application US/09414878

Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-65

Query Match 44.0%; Score 201; DB 3; Length 58;
Best Local Similarity 61.8%; Pred. No. 9,1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 27 RDPFCELPADTGPCRVPRFPSPFYNNPDEKCLBEFYGGCGGNNNFTLKECESTC 81
DB 1 KDFPCELBEDTGPCRGFRFPRFYNNOTKOCFTFYGGCGGNNNFTLKECKNIC 55

RESULT 12
US-09-240-136-65
Sequence 65, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William

APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-65

Query Match 44.0%; Score 201; DB 3; Length 58;
Best Local Similarity 61.8%; Pred. No. 9,1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 27 RDPFCELPADTGPCRVPRFPSPFYNNPDEKCLBEFYGGCGGNNNFTLKECESTC 81
DB 1 KDFPCELBEDTGPCRGFRFPRFYNNOTKOCFTFYGGCGGNNNFTLKECKNIC 55

RESULT 13
US-09-638-770A-65
Sequence 65, Application US/09638770A
Patent No. 6423498
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P.
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DXX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-638-770A-65
Query Match 44.0%; Score 201; DB 4; Length 58;
Best Local Similarity 61.8%; Pred. No. 9.1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY 27 RPPDFCELPADTGPGRVPRPSFYNNPDEKCKLEFIYGGCGGNANFTKECESTCA 81
DB 1 KPPDFCELPEDTGPGRGRFDRIFNNQKCTFIYGGCGGNANFTKECESTCA 55
RESULT 14
US-08-358-160-91
Sequence 91, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iyer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-91
Query Match 44.0%; Score 201; DB 1; Length 61;
Best Local Similarity 57.6%; Pred. No. 9.6e-18;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
QY 25 KDRPDFCELPADTGPGRVPRPSFYNNPDEKCKLEFIYGGCGGNANFTKECESTCA 83
DB 1 QDRPKFCELPADTGPGRCAHIFRYFYDSASNNKNNFTYGGCGGNANFTKECESTCA 59
RESULT 15
US-08-358-160-94
Sequence 94, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160
 FILING DATE: 16-DEC-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/133,031
 FILING DATE: 13-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,319
 FILING DATE: 26-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/664,989
 FILING DATE: 01-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/487,063
 FILING DATE: 02-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/240,160
 FILING DATE: 02-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: 187-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-358-160-94

Query Match: 43.3%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 2,1e-17;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 27 RPDPELADDTGCPVRFPSFYNPDEKKLEPTIGGCGGNANRFTKECESTC 81
 Db 1 RPDPELADDTGCPVRFPSFYNPDEKKLEPTIGGCGGNANRFTKECESTC 55

Search completed: January 23, 2004, 10:29:11
 Job time : 13.7359 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 40.0387 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179a-16
Perfect score: 457
Sequence: 1 MESSGILLILGILLTWEVL.....CEGANNPIKESCESTCAA 83

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:	Query	Match	Length	DB	ID	Description
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:**	457	100.0	83	21	AAV15145	Proform of Txln 1
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:**	438	95.8	83	21	AAV15146	Proform of Txln 2
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:**	361	79.0	83	21	AAV15147	Proform of Txln 3
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:**	343	75.1	83	21	AAV15150	Proform of Txln 6
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:**	342	74.8	83	21	AAV15149	Proform of Txln 5
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:**	341	74.6	59	21	AAV15138	Txln 1 Plasmid inh
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:**	334	73.1	60	21	AAV15148	Proform of Txln 4
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:**	334	73.1	60	21	AAV15153	Plasmid Inhibitor
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:**	322	70.5	59	21	AAV15139	Txln 2 Plasmid inh

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	299	65.4	60	21	AAV15151	Plasmin Inhibitor
11	298	65.2	60	21	AAV15154	Plasmin Inhibitor
12	245	53.6	59	21	AAV15140	Txln 3 Plasmin inh
13	227	49.7	59	21	AAV15143	Txln 6 Plasmin inh
14	226	49.5	59	21	AAV15142	Txln 5 Plasmin inh
15	225	49.2	59	21	AAV15141	Txln 4 Plasmin inh
16	221	48.4	58	17	AAV15146	Aprotinin-like Kun
17	201	44.0	58	16	AAV178542	Human LACI-K2 deri
18	196	42.9	58	16	AAV178546	Human collagen alp
19	192	42.0	58	16	AAV178552	Human TFP1-2 domai
20	189	41.4	58	16	AAV178544	Human LACI-K3 deri
21	185.5	40.6	145	18	AAV25935	Novel protease inh
22	185.5	40.6	165	18	AAV25937	Elastase inhibitor
23	185	40.5	86	22	AAV25938	I. ricinus salivar
24	185	40.5	124	18	AAV25933	New protease inh
25	185	40.5	144	18	AAV25938	SUC2-Ep7-d21-RPDE
26	184	40.5	58	17	AAV25937	Genetically engine
27	183	40.0	55	18	AAV25931	RPDE-Kunitz domain
28	183	40.0	124	18	AAV25932	New protease inh
29	183	40.0	144	18	AAV25936	SUC2-Ep1-d21-RPDE
30	182	39.8	58	17	AAV25938	Genetically engine
31	182	39.8	58	17	AAV25938	Genetically engine
32	181	39.6	58	13	AAV27492	Human neutrophil e
33	181	39.6	58	17	AAV259159	Genetically engine
34	181	39.6	58	17	AAV259160	Genetically engine
35	181	39.6	252	22	AAV259286	Kunitz type 2 Ser
36	180	39.4	58	13	AAV27396	Human neutrophil e
37	180	39.4	58	17	AAV259191	Genetically engine
38	180	39.4	58	17	AAV259184	Genetically engine
39	180	39.4	240	21	AAV30045	Human placental bi
40	180	39.4	240	21	AAV30045	Human placental bi
41	180	39.4	252	18	AAV30040	Human placental bi
42	180	39.4	252	18	AAV30040	Hepatocyte growth
43	180	39.4	252	19	AAV70286	Human tissue facto
44	180	39.4	252	21	AAV70286	Human kunitz type
45	180	39.4	252	21	AAV70286	Human placental bi

ALIGNMENTS

RESULT 1	AAV15145	AAV15145 standard; Protein; 83 AA.
AC	AAV15145;	
XX		
DT	07-FEB-2000 (first entry)	
XX		
DE	Proform of Txln 1 protein.	
XX		
KW	Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;	
KW	Australian brown snake; conserved cysteine residue; stability; Aprotinin;	
KW	haematopoietic; cytosolic activity; homology; specificity; control;	
KW	Tatcoctoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;	
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;	
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;	
KW	reduced propensity; chromosis.	
XX		
OS	Pseudonaja textilis textilis.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..24
FT	Protein	/label= Leader_peptide
FT		25..83
FT		/label= Txln-1-protein
XX		/note= "Textilinin-1"
XX		
XX	W0958569-A1.	
XX		
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999; .99WO-AU00343.	

```

XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAF/) GAFNEY P J.
XX
XX Maaci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV,
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229024.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40a; Page 71; 112pp; English.
XX
XX The present sequence is the proform of the Textillinin protein, Txln 1,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
XX 58% homology with Aprotinin and Talicotoxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 100.0%; Score 457; DB 21; Length 83;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-46;
XX Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGLLLLLGLTMEVLTTPVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPI 60
XX DB 1 MSSGGLLLLLGLTMEVLTTPVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPI 60
XX
XX QY 61 YGGCGNNANPITKECESTCA 83
XX DB 61 YGGCGNNANPITKECESTCA 83
XX
XX RESULT 2
XX AAY15146
XX ID AAY15146 standard; Protein; 83 AA.
XX AC AAY15146;
XX XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 2 protein.
XX
XX Textillinin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
XX haematopoietic; cytostatic activity; homology; specificity; control;
XX Talicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX FT /label= Leader_peptide
XX FT 25..83
XX FT Protein
XX /label= Txln-2_protein

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FT /note= "Textillinin-2"
XX
XX PN MO958569-A1.
XX
XX PD 18-NOV-1999.
XX
XX PF 07-MAY-1999; 99MO-AU00343.
XX
XX PR 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAF/) GAFNEY P J.
XX
XX Maaci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV,
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229025.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40b; Page 71; 112pp; English.
XX
XX The present sequence is the proform of the Textillinin protein, Txln 2,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln 2 has 43% and
XX 55% homology with Aprotinin and Talicotoxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 95.8%; Score 438; DB 21; Length 83;
XX Best Local Similarity 95.2%; Pred. No. 2.2e-44;
XX Matches 79; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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XX QY 1 MSSGGLLLLLGLTMEVLTTPVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPI 60
XX DB 1 MSSGGLLLLLGLTMEVLTTPVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPI 60
XX
XX QY 61 YGGCGNNANPITKECESTCA 83
XX DB 61 YGGCGNNANPITKECESTCA 83
XX
XX RESULT 3
XX AAY15147
XX ID AAY15147 standard; Protein; 83 AA.
XX AC AAY15147;
XX XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 3 protein.
XX
XX Textillinin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.

```

```

XX Key Location/Qualifiers
PH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-3 protein
FT /note= "Textilinin-3"
XX
XX MO9958569-A1.
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M P.
XX (GAFV/) GAFNEY P J.
XX
XX Maeti PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29026.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40c; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 3,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX SQ Sequence 83 AA;
XX
XX Query Match 79.0%; Score 361; DB 21; Length 83;
XX Best Local Similarity 77.1%; Pred. No. 3.2e-35;
XX Matches 64; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGLILLLGLTLTMEVLTTPVSSKDRPFCPLPADTGCRVRFPSPYNNPEKKCLAEFI 60
XX DB 1 MSSGGLILLLGLTLTMEVLTTPVSSKDRPFCPLPADTGCRVCKNKIKRFFYNNPQHCIEFL 60
XX
XX QY 61 YGGCGNNANFTKECESTCA 83
XX DB 61 YGGCGNNANFTKECESTCA 83
XX
XX RESULT 4
XX ID AAY15150 standard; Protein; 83 AA.
XX AC AAY15150;
XX DT 07-FEB-2000 (first entry)
XX DE Proform of Txln 6 protein.
XX
XX Textilinin proform; Txln 6; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;

```

```

XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
PH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-6 protein
FT /note= "Textilinin-6"
XX
XX MO9958569-A1.
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M P.
XX (GAFV/) GAFNEY P J.
XX
XX Maeti PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29029.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40f; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 6,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX SQ Sequence 83 AA;
XX
XX Query Match 75.1%; Score 343; DB 21; Length 83;
XX Best Local Similarity 77.1%; Pred. No. 4.5e-33;
XX Matches 64; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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XX QY 1 MSSGGLILLLGLTLTMEVLTTPVSSKDRPFCPLPADTGCRVRFPSPYNNPEKKCLAEFI 60
XX DB 1 MSSGGLILLLGLTLTMEVLTTPVSSKDRPFCPLPADTGCRVDFGTAFHSPREHECIEFI 60
XX
XX QY 61 YGGCGNNANFTKECESTCA 83
XX DB 61 YGGCGNNANFTKECESTCA 83
XX
XX RESULT 5
XX ID AAY15149 standard; Protein; 83 AA.
XX AC AAY15149;
XX DT 07-FEB-2000 (first entry)
XX

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DE Perform of Txln 5 protein.

XX
XX
KW Textillinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW reduced propensity; thrombosis.

XX
OS Pseudonaja textilis textilis.

XX
FH Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader_peptide
FT 25..83
FT Protein /label= Txln-5 Protein
FT /note= "Textillinin-5"

XX
PN WO958569-A1.

XX
PD 18-NOV-1999.

XX
PF 07-MAY-1999; 99WO-AU00343.

XX
PR 11-MAY-1998; 98AU-0003450.

XX
PA (UYOU) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASC P P.
PA (LAVI/) LAVIN M P.
PA (GAFV/) GAFNEY P J.

XX
PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI, 2000-039073/03.
XX DR N-PSDB; AA229028.

XX
PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -

XX
PS Claim 40e; Page 72; 112pp; English.

XX
CC The present sequence is the proform of the Textillinin protein, Txln 5,
CC that is a single stage competitive inhibitor of plasmin. It is isolated
CC from the Australian brown snake, Pseudonaja textilis textilis. It has
CC six conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln has high
CC specificity for plasmin and low inhibitory efficiency, that can
CC transiently affect the delicate balance between enzymes and inhibitors
CC of the fibrinolytic system, controlling the fluidity of blood. The
CC plasmin inhibitors are useful for alleviating blood loss, following
CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC propensity to cause thrombosis.

XX
SQ Sequence 83 AA;

Query Match 74.8%; Score 342; DB 21; Length 83;
Best Local Similarity 77.1%; Pred. No. 5; 9e-33;
Matches 64; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSSGGLLILGLITLMEVLTVPSSKDRPDCRLPADTGCRVAFPSFYNPDPKCKLEFI 60
DB 1 MSSGGLLILGLITLMEVLTVPSSKDRPDCRLPADTGCRVAFPSFYNPDPKCKLEFI 60

QY 61 YGCGEGNANNFITKECESTCA 83
DB 61 YGCGEGNANNFITKECESTCA 83

RESULT 6
AAV15138
ID AAV15138 standard; Protein; 59 AA.

XX
AC AAV15138;
XX
DT 07-FEB-2000 (first entry)

XX
DE Txln 1 Plasmin inhibitor protein.

XX
KW Textillinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytostatic activity; homology; specificity; Apoptin;
KW Talocotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW reduced propensity; thrombosis.

XX
OS Pseudonaja textilis textilis.

XX
PN WO958569-A1.

XX
PD 18-NOV-1999.

XX
PF 07-MAY-1999; 99WO-AU00343.

XX
PR 11-MAY-1998; 98AU-0003450.

XX
PA (UYOU) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASC P P.
PA (LAVI/) LAVIN M P.
PA (GAFV/) GAFNEY P J.

XX
PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI, 2000-039073/03.
XX DR N-PSDB; AA229017.

XX
PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -

XX
PS Claim 8a; Page 68; 112pp; English.

XX
CC The present sequence is the Textillinin protein, Txln 1, that is a
CC single stage competitive inhibitor of plasmin. It is isolated from the
CC Australian brown snake, Pseudonaja textilis textilis. It has six
CC conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
CC 58% homology with Apoptin and Talocotoxin-associated plasmin inhibitor
CC (TAC), respectively. Txln has high specificity for plasmin and low
CC inhibitory efficiency, that can transiently affect the delicate balance
CC between enzymes and inhibitors of the fibrinolytic system, controlling
CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
CC blood loss, following major surgery or trauma. Conjugates of the plasmin
CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
CC They have reduced propensity to cause thrombosis.

XX
SQ Sequence 59 AA;

Query Match 74.6%; Score 341; DB 21; Length 59;
Best Local Similarity 100.0%; Pred. No. 5; 2e-33;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 KDRPDCRLPADTGCRVAFPSFYNPDPKCKLEFIYGGCGNANNFITKECESTCA 83
DB 1 KDRPDCRLPADTGCRVAFPSFYNPDPKCKLEFIYGGCGNANNFITKECESTCA 59

RESULT 7
AAV15148
ID AAV15148 standard; Protein; 83 AA.

XX
AC AAV15148;
XX
DT 07-FEB-2000 (first entry)

XX DE Proform of Txln 4 protein.
 XX XX
 KM Textillinin proform; Txln 4; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugates; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX OS
 XX Pseudonaja textilis textilis.
 XX XX
 FH Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader_peptide
 FT Protein 25..83
 FT /label= Txln-4 protein
 FT /note= "Textillinin-4"
 XX XX
 PN MO9958569-A1.
 XX PD 18-NOV-1999.
 XX PP 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.
 XX XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAPF/) GAFNEY P J.
 XX PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ20927.
 XX XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX XX
 PS Claim 40d; Page 72; 112pp; English.
 XX XX
 CC The present sequence is the proform of the Textillinin protein, Txln 4,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC XX
 SQ Sequence 83 AA;
 Query Match 74.6%; Score 341; DB 21; Length 83;
 Best Local Similarity 77.1%; Pred. No. 7.7e-33;
 Matches 64; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 MSSGGLLLLLGLITTWVLTTPVSSKDRPFCPLPADTGCRCRFRPFYNNPBEKCLEFTI 60
 Db 1 MSSGGLLLLLGLITTWVLTTPVSSKDRPFCPLPADTGCRCRFRPFYNNPBEKCLEFTI 60
 Oy 61 YGCGGNANNTTKKECESTCAA 83
 Db 61 YGCGGNANNTTKKECESTCAA 83
 RESULT 8
 AAY15153

ID AAY15153 standard; Protein; 60 AA.
 XX AC AAY15153;
 XX XX
 DT 07-FEB-2000 (first entry)
 XX XX
 DE Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.
 KM Textillinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; homology; specificity; enzyme;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 KM fibrinolytic system; conjugates; anti-fibrin antibody; anti-tumour agent;
 KM inhibitory efficiency; reduced propensity; thrombosis.
 XX OS
 XX Pseudonaja textilis textilis.
 XX XX
 FH Key Location/Qualifiers
 FH Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 47
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"
 XX XX
 PN MO9958569-A1.
 XX PD 18-NOV-1999.
 XX PP 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.
 XX XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAPF/) GAFNEY P J.
 XX PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29047.
 XX XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX XX
 PS Disclosure; Fig 6; 112pp; English.
 XX XX
 CC The present amino acid sequence is the Txln 1, Textillinin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC XX
 SQ Sequence 60 AA;
 Query Match 73.1%; Score 334; DB 21; Length 60;
 Best Local Similarity 96.6%; Pred. No. 3.6e-32;
 Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 25 KDRPFCPLPADTGCRCRFRPFYNNPBEKCLEFTIYGCGGNANNTTKKECESTCAA 83
 Db 2 KDRPFCPLPADTGCRCRFRPFYNNPBEKCLEFTIYGCGGNANNTTKKECESTCGS 60
 RESULT 9
 AAY15139

ID AAY15139 standard; Protein; 59 AA.
 AC AAY15139;
 XX
 DT 07-FEB-2000 (first entry)
 DE Txln 2 Plasmin inhibitor protein.
 XX
 XX Textilin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; homology; specificity; Apoptin;
 KM Talcotoxin-associated plasmin inhibitor; TAC; inhibitor efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PE 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI, 2000-039073/03.
 DR N-PSDB; AA229018.
 DR
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PT
 PS Claim 8b; Page 69; 112pp; English.
 XX
 CC The present sequence is the Textilin protein, Txln 2 that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln 2 has 43% and
 CC 55% homology with Apoptin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX
 SQ Sequence 59 AA;
 Query Match 70.5%; Score 322; DB 21; Length 59;
 Best Local Similarity 93.2%; Pred. No. 9.4e-11;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 25 KDRPFCRLPAPDTPGCRVPPSPFYNNPDKKLCLEFTYGGCEGNANFTKECESTCAA 83
 DB 1 KDRPFCRLPAPDTPGCRVPPSPFYNNPDKKLCLEFTYGGCEGNANFTKECESTCAA 59
 RESULT 10
 ID AAY15151 standard; Protein; 60 AA.
 AC AAY15151;
 XX

DT 07-FEB-2000 (first entry)
 XX
 XX Plasmin inhibitor Txln 1, partial protein sequence.
 XX
 KM Textilin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitor efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM rapid amplification of cDNA end; RACE; reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein 25..60
 FT /label= Leader_peptide
 FT /label= Partial_Txln-1_protein
 FT /note= "Plasmin inhibitor"
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PE 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI, 2000-039073/03.
 DR N-PSDB; AA229030.
 DR
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PT
 PS Example 2; Page 108; 112pp; English.
 XX
 CC The present sequence is the partial Txln 1, Textilin protein sequence.
 CC It is obtained by sequence analysis of the 5' and 3' RACE products. It is
 CC a single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln 1 has 45% and
 CC 58% homology with Apoptin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX
 SQ Sequence 60 AA;
 Query Match 65.4%; Score 299; DB 21; Length 60;
 Best Local Similarity 91.7%; Pred. No. 5.3e-28;
 Matches 55; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPFCRLPADTGRCRVFPSPFYNNPDKKLCLEFT 60
 DB 1 MSSGILLILGLITLMEVLTTPVSSKDRPFCRLPADTGRCRVFPSPFYNNPDKKLCLEFT 60
 RESULT 11
 ID AAY15154 standard; Protein; 60 AA.
 AC AAY15154;
 XX

AC	AAV15154;
XX	
DT	07-FEB-2000 (first entry)
DE	
XX	
XX	plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
KM	
KW	Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
KX	Australian brown snake; conserved cysteine residue; stability; control;
KM	haemastopoletic; cytosolic activity; homology; enzyme;
KW	fuidity of blood; alleviate; blood loss; major surgery; trauma;
KX	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX	inhibitory efficiency; reduced propensity; thrombosis.
OS	
XX	Pseudonaja textilis textilis.
XX	
Key	Location/Qualifiers
FH	Misc-difference 24
FT	/note= "encoded by TNG"
FT	Misc-difference 45
FT	/note= "encoded by GAT"
FT	Misc-difference 49
FT	/note= "encoded by ATG"
FT	Misc-difference 59
FT	/note= "encoded by CGN"
PN	WO958569-A1.
PD	18-NOV-1999.
XX	
XX	07-MAY-1999; 99WO-AU00343.
XX	
PR	11-MAY-1998; 98AU-0003450.
XX	
PA	(UYOU) UNIT QUEENSLAND.
PA	(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA	(MASC/) MASI P P.
PA	(LAVI/) LAVIN M F.
PA	(GAFF/) GAFFNEY P J.
XX	
PI	Mascl PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
DR	WPI; 2000-039073/03.
DR	N-PSDB; AAZ29048.
PT	Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT	agents -
XX	
PS	Disclosure; Fig 7; 112pp; English.
XX	
CC	The present amino acid sequence is the Txln 2, Textillin protein
CC	inhibited by the partial cDNA sequence. It is a single stage competitive
CC	inhibitor of plasmin. It is isolated from the Australian brown snake,
CC	Pseudonaja textilis textilis. Txln has high specificity for plasmin and
CC	low inhibitory efficiency that can transiently affect the delicate
CC	balance between enzymes and inhibitors of the fibrinolytic system,
CC	controlling the fluidity of blood. The plasmin inhibitors are useful for
CC	alleviating blood loss, following major surgery or trauma. Conjugates of
CC	the plasmin inhibitor and an anti-fibrin antibody are useful as
CC	anti-tumour agents. They have reduced propensity to cause thrombosis.
XX	
SQ	Sequence 60 AA;
Query Match	65.2%; Score 298; DB 21; Length 60;
Best Local Similarity	89.5%; Pred. No. 6, 9e-28;
Matches 51; Conservative	2; Mismatches 4; Indels 0; Gaps 0
OY	25 KDRPFCPLADTGPCRVFPSPFYNNPEKKCLERITYGGCGEANNPFITKBCSTC 81 Dd 2 KDRPFLCHLPDTGCRVRFPSPFYNNPBOKCLFRITYGCENANNAFITKBCSTC 58
RESULT 12	

ID	AAV15140
AC	AAV15140; standard; Protein; 59 AA.
DT	07-FEB-2000 (first entry)
DE	Txln 3 Plasmin inhibitor protein.
KW	Textillinin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
KW	Australian brown snake; conserved cysteine residue; stability; control;
KW	haemostatic; cytosolic activity; specificity; inhibitory efficiency;
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW	reduced propensity; thrombosis.
OS	Pseudonaja textilis textilis.
PN	MO9958569-A1.
PD	18-NOV-1999.
PP	07-MAY-1999; 99WO-AU00343.
PR	11-MAY-1998; 98AU-0003450.
PA	(YOU) UNIV QUEENSLAND.
PA	(NAB-) NAT INST BIOLOGICAL STANDARDS & CO.
PA	(MASC/) MASI P P.
PA	(LAVI/) LAVIN M F.
PA	(GAF/) GAFNEY P J.
PI	Masi PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV,
DR	WPI: 2000-039073/03.
DR	N-PSDB; AAZ29019.
PT	Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT	agents -
PS	Claim 8c; Page 69; 112pp; English.
CC	The present sequence is the Textillinin protein, Txln 3, that is a
CC	single stage competitive inhibitor of plasmin. It is isolated from the
CC	Australian brown snake, Pseudonaja textilis textilis. It has six
CC	conserved cysteine residues, that endow them great stability. This
CC	sequence has haemostatic and cytotoxic activity. Txln has high
CC	specificity for plasmin and low inhibitory efficiency, that can
CC	transiently affect the delicate balance between enzymes and inhibitors
CC	of the fibrinolytic system, controlling the fluidity of blood. The
CC	plasmin inhibitors are useful for alleviating blood loss, following
CC	major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC	anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC	propensity to cause thrombosis.
SQ	Sequence 59 AA:
Query Match	53.6%; Score 245; DB 21; Length 59;
Best Local Similarity	67.8%; Pred.No.1.4e-21;
Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0	
25 KDRPDPFELPADNGPCRVRRPSPFTYNDPEKKCLEPTYGCGCGNANNTTKECESTCA 83	: : :
1 KDRNPCKLPATGRCNAKITRFYYNPROHCIEFLYGGCGGNANNFXTIKCESTCAA 59	: : :
RESULT 13	
ID	AAV15143
AC	AAV15143; standard; Protein; 59 AA.
DT	07-FEB-2000 (first entry)

XX Txln 6 Plasmin inhibitor protein.
 XX
 XX Textilin protein; Txln 6; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 XX Pseudonaja textilis textilis.
 OS
 XX W09958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 XX
 XX (UYOU) UNIV QUEENSLAND.
 XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 XX (MASC/) MASI P P.
 XX (LAVI/) LAVIN M F.
 XX (GAFV/) GAFNEY P J.
 XX
 XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI: 2000-039073/03.
 XX N-PDB; AA229022.
 XX
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Claim 8f; Page 69; 112pp; English.
 PS
 XX The present sequence is the Textilin protein, Txln 6, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 XX Sequence 59 AA;
 SQ
 Query Match 49.7%; Score 227; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 1.9e-19;
 Matches 40; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 Oy 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 83
 ID AAY15142 standard; Protein; 59 AA.
 XX
 XX AAY15142;
 AC
 XX 07-FEB-2000 (first entry)
 DT
 XX Txln 5 Plasmin inhibitor protein.
 DE
 XX Textilin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM reduced propensity; thrombosis.

KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 XX Pseudonaja textilis textilis.
 OS
 XX W09958569-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 XX
 XX (UYOU) UNIV QUEENSLAND.
 XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 XX (MASC/) MASI P P.
 XX (LAVI/) LAVIN M F.
 XX (GAFV/) GAFNEY P J.
 XX
 XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI: 2000-039073/03.
 XX N-PDB; AA229021.
 XX
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Claim 8e; Page 69; 112pp; English.
 PS
 XX The present sequence is the Textilin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 XX Sequence 59 AA;
 SQ
 Query Match 49.5%; Score 226; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 2.5e-19;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 Oy 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 83
 ID AAY15141 standard; Protein; 59 AA.
 XX
 XX AAY15141;
 AC
 XX 07-FEB-2000 (first entry)
 DT
 XX Txln 4 Plasmin inhibitor protein.
 DE
 XX Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 XX Pseudonaja textilis textilis.

PN WO958569-A1.
 XX 18-NOV-1999.
 PD 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAF/) GAFNEY P J.
 XX
 PI Masci PF, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,
 XX WPI, 2000-039073/03.
 DR N-PSDB; AA229020.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 XX
 PS Claim 8d; Page 69; 112pp; English.
 CC The present sequence is the Textillin protein, Txln 4, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 XX
 SQ Sequence 59 AA;

Query Match 49.2%; Score 225; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 3.3e-19;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 25 KDRPDPCELPADTGPCRVRFPSFYNNPDEKCLERIVGCGGNANNFITKEBCESTCA 83
 DB 1 KDRPKPCBLPASTGCKGNVPRFTYNADHQLKFTYGGCGGNANNFITBEGKSTCA 59

Search completed: January 23, 2004, 10:24:36
 Job time : 41.0387 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 5.40141 Seconds

(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179A-8

Sequence: 1 KDHPKFCFLPAETGSCCKGNV.....CGNANNFKTIEBCKSTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	65.5	61	1	P00991 vipera ammo
2	212	62.0	57	1	P20229 naja naja (
3	212	62.0	65	1	P25660 bungarus fa
4	209	61.1	57	1	P00986 naja nivea
5	207	60.5	57	1	P00985 hemachatus
6	207	60.5	65	1	P00992 vipera ammo
7	192	56.1	58	1	P25966 ophiophagus
8	189	55.3	62	1	P24541 elapscophi
9	186	54.4	60	1	P00990 dabola rusa
10	184	53.8	62	1	P10280 anemolia su
11	178	52.0	57	1	P00981 dendroaspis
12	178	52.0	57	1	P00982 dendroaspis
13	172	50.3	55	1	P81902 bombyx mori
14	172	50.3	55	1	P00981 dendroaspis
15	172	50.3	55	1	P00982 dendroaspis
16	168	49.1	304	1	P00984 dendroaspis
17	167	48.8	58	1	P00984 dendroaspis
18	166	48.5	55	1	P31713 sciochiactis
19	165	48.2	55	1	P02445 rattus norv
20	165	48.2	110	1	P81129 sciochiactis
21	165	48.2	300	1	P00979 dendroaspis
22	164	48.0	58	1	P19761 oryctolagus
23	161	47.1	304	1	P19761 oryctolagus
24	157	45.9	57	1	P19855 naja naja (
25	157	45.9	306	1	P19855 naja naja (
26	155	45.3	58	1	P00980 dendroaspis
27	153	44.7	59	1	P00980 dendroaspis
28	150	43.9	60	1	P00979 dendroaspis
29	150	43.9	235	1	P48307 homo sapien
30	149	43.6	230	1	O35536 mus musculu
31	147	43.0	69	1	P81162 boophilus m
32	146	42.7	102	1	Q23143 trichosurus
33	144.5	42.3	197	1	P82968 melittina c

34	143	41.8	100	1	BPT1_BOVIN	P00974 bos taurus
35	143	41.8	507	1	SPT1_MOUSE	Q91977 mus musculu
36	141	41.2	60	1	IBS1_BOVIN	P00975 bos taurus
37	141	41.2	60	1	TXCA_DENAN	P81658 dendroaspis
38	141	41.2	763	1	APP2_HUMAN	Q06481 homo sapien
39	140	40.9	57	1	IVB1_DENAN	P00983 dendroaspis
40	140	40.9	351	1	TKD1_BOVIN	Q28201 bos taurus
41	139	40.6	770	1	A4_MOUSE	P12023 m amyloid b
42	138	40.4	100	1	BPT2_BOVIN	P04815 bos taurus
43	138	40.4	765	1	APP2_RAT	P15943 rattus norv
44	137	40.1	76	1	A4_MACMU	P29216 macaca mula
45	137	40.1	252	1	SPT2_HUMAN	O43291 homo sapien

ALIGNMENTS

RESULT 1	IBV1_VIPAA	STANDARD;	PRT;	61 AA.
ID	P00991			
AC	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom basic protease inhibitor I (Venom trypsin inhibitor I)			
OS	Vipera ammodytes ammodytes (Western sand viper)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Leptodactyla; Squamata; Chordata; Serpentes; Colubroidae;			
OC	Viperidae; Viperinae; Vipera.			
OX	NCBI_TaxID=8705;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RA	MEDLINE=84053385; PubMed=6639951;			
RT	Rictonia A., Meloun B., Gubensek P.;			
RT	"The primary structure of Vipera ammodytes venom trypsin inhibitor			
RT	I."			
CC	-1- FUNCTION: This protein inhibits trypsin and kallikrein.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01222; TIVITI.			
DR	HSSP; P31713; ISHP.			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI_1.			
DR	Pfam; PF000222; Kunitz_BPTI_1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 1.			
KW	Serine protease inhibitor; Pyroglutamate carboxylic acid.			
FT	MOD RES	1	57	
FT	DISULFID	7	57	
FT	DISULFID	16	40	
FT	DISULFID	32	53	
FT	DISULFID	32	53	
SO	SEQUENCE	61 AA;	6865 MW;	FC8285F579FE3795 CRC64;
Query Match		65.5%;	Score 224;	DB 1; Length 61;
Best Local Similarity		62.7%;	Freq. No. 7.2e-20;	
Matches	37;	Conservative 10;	Mismatches 12;	Indels 0;
Gaps	0;			
Qy	1 KDHPKFCFLPAETGSCCKGNVPRFYNNADHOCLEKRYGCGGANNFKTIEBCKSTCAA 59			
Db	1 QDHPKFCFLPAETGSCCKGNVPRFYNNADHOCLEKRYGCGGANNFKTIEBCKSTCAA 59			
RESULT 2	IBV1_NAJNA	STANDARD;	PRT;	57 AA.
ID	P20229			
AC	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom trypsin inhibitor.			

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OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bapinae; Naja.
NCBI_TaxID=35670;
OK NCBI_TaxID=35670;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91099304; PubMed=1702706;
RA Shafat J., Beg O.U., Yin S.-J., Zaidi Z.H., Joernvall H.;
RT "Primary structure and functional properties of cobra (Naja naja
naia) venom kunitz-type trypsin inhibitor.";
RL Eur. J. Biochem. 194;337-341(1990).
CC -1- FUNCTION: This protein inhibits trypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR, S13846; S13846.
DR HSSP, P00981; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR PRINTS, PR00759; BASICPTASE.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6371 MW; AABPD72949ADCL2A CRC64;

Query Match 62.0%; Score 212; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 1,7e-18;
Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 PKFCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 57
DB 2 PKFCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 55

RESULT 3
ID IVB1_BUNFA STANDARD; PRT; 65 AA.
AC P25660;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitors IX and VIIIB.
OS Bungarus fasciatus (Banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
NCBI_TaxID=8613;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=83160048; PubMed=6832893;
RA Liu C.-S., Wu T.-C., Lo T.-B.;
RT "Complete amino acid sequences of two protease inhibitors in the
venom of Bungarus fasciatus.";
RL Int. J. Pept. Protein Res. 21:209-215(1983).
CC -1- FUNCTION: Inhibitor of chymotrypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP, P00980; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR PRINTS, PR00759; BASICPTASE.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE, PS50279; BPTI_KUNITZ_2; 1.

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KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
FT ACT SITE 63 65 MISSING (IN INHIBITOR VIIIB).
SQ SEQUENCE 65 AA; 7294 MW; BAJ40749E194DB51 CRC64;

Query Match 62.0%; Score 212; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 2e-18;
Matches 37; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 KDPKCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTCA 59
DB 1 KDPKCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTCA 59

RESULT 4
ID IVB2_NAJNI STANDARD; PRT; 57 AA.
AC P00986;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja naja (Cape cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bapinae; Naja.
NCBI_TaxID=8655;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76237547; PubMed=950337;
RA Hokana Y., Iwanaga S., Tatsuki T., Suzuki T.;
RT "Snake venom protease inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
(Ringhals cobra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them.";
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
that of bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP, P00981; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 61.1%; Score 209; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 3.9e-18;
Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 4 PKFCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 57
DB 2 PKFCELPATGSGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 55

RESULT 5
ID IVB2_HEMHA STANDARD; PRT; 57 AA.
AC P00985;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Ringhale) (Sepedon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Hemachatus.
 NCBI_TaxID=8626;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokana Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Ringhale's cobra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them."
 RL J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC -1- bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01216; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7E2A CRC64;
 Query Match 60.5%; Score 207; DB 1; Length 57;
 Best Local Similarity 66.7%; Pred. No. 6.7e-18; Indels 0; Gaps 0;
 Matches 36; Conservative 5; Mismatches 13;
 QY 4 PKFCELPALPTGSCGKGNVPRFYNNADHQCLEFIYGGCGGNANKRTIEGKSTC 57
 DB 2 PKFCELPALPTGTCRAVYIRSFHYNLAQCQIFIVGGCGGNANKRPTIDECHRTIC 55
 RESULT 6
 ID IVB3 VIPAA STANDARD; PRT; 65 AA.
 AC P00952;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Viperinae.
 NCBI_TaxID=8705;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Ritonja A., Meloun B., Gubensek F.;
 RT "The primary structure of Viperinae venom chymotrypsin
 RT inhibitor."
 RL Biochim. Biophys. Acta 746:138-145(1983).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01223; TIVIVC.
 DR HSSP; P31713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17 18
 SQ SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;
 Query Match 60.5%; Score 207; DB 1; Length 65;
 Best Local Similarity 61.0%; Pred. No. 7.7e-18; Indels 0; Gaps 0;
 Matches 36; Conservative 7; Mismatches 16;
 QY 1 KDHPKCELPALPTGSCGKGNVPRFYNNADHQCLEFIYGGCGGNANKRTIEGKSTCA 59
 DB 1 RDRPKFCELPALPTGRCCLAVNPRFYNNASNKCEKFEIYGGCGGNANKRPTMECHRTICVA 59
 RESULT 7
 ID IVBC OPHNA STANDARD; PRT; 58 AA.
 AC P82966;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom chymotrypsin inhibitor.
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Ophiophagus.
 NCBI_TaxID=8665;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=21248396; PubMed=11350064;
 RA Chang L.-S., Chung C., Huang H.-B., Lin S.-R.;
 RT "Purification and characterization of a chymotrypsin inhibitor from
 RT the venom of Ophiophagus hannah (King Cobra)."
 RL Biochem. Biophys. Res. Commun. 283:862-867(2001).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P00981; IDTK.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IDA.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 6 56 BY SIMILARITY.
 FT DISULFID 15 39 BY SIMILARITY.
 FT DISULFID 31 52 BY SIMILARITY.
 FT ACT SITE 16 17 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 58 AA; 6499 MW; 3EB44C85F0843D8A CRC64;
 Query Match 56.1%; Score 192; DB 1; Length 58;
 Best Local Similarity 63.0%; Pred. No. 4e-16; Indels 0; Gaps 0;
 Matches 34; Conservative 2; Mismatches 18;
 QY 4 PKFCELPALPTGSCGKGNVPRFYNNADHQCLEFIYGGCGGNANKRTIEGKSTC 57
 DB 3 PKFCELPALPTGRCCLAVNPRFYNNASNKCEKFEIYGGCGGNANKRPTIDECHRTIC 56
 RESULT 8
 ID IVBT ERIMA STANDARD; PRT; 62 AA.
 AC P24511;

DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis machanoni (leaf-nosed viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Eristocophis.
 OX NCBI_TaxID=8702;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddig A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 from leaf-nosed viper venom."
 RL FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: S19327; S19327.
 DR HSSP; P00381; 1DVK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Serine protease inhibitor.
 FT DISULFID 2 52 BY SIMILARITY.
 FT DISULFID 11 35 BY SIMILARITY.
 FT ACT SITE 27 48 BY SIMILARITY.
 FT ACT SITE 12 13 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6772 MW; 0A2BD0AD20DP938 CRC64;

Query Match
 Best Local Similarity 55.3%; Score 189; DB 1; Length 62;
 Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 6 FCELPATGSCGVNPRFYTNADHOCLEFYGGCGGANNFTIEGKSTCA 59
 DB 1 FCELPDPCVCKAHIPFYTNPNASKCKNFIYGGCGGANNFTIEGKSTCA 54
 RESULT 9
 IYB2_DABRU STANDARD; PRT; 60 AA.
 AC P00950;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II (RVV-II).
 OS Daboia russelii stanselii (Siamese Russell's viper) (Vipera russelii
 siamensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Daboia.
 OX NCBI_TaxID=8708;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=75060360; PubMed=4436285;
 RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
 RT "Snake venom proteinase inhibitor, II. Chemical structure of
 inhibitor II isolated from the venom of Russell's viper (Vipera
 russelii)." ;
 RT J. Biochem. 76:721-733(1974).
 CC -1- FUNCTION: This inhibitor has activity similar to bovine basic
 protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P10646; 1ADZ.

DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17* 18
 SQ SEQUENCE 60 AA; 6850 MW; 5A7DCE9554CE6E82 CRC64;

Query Match
 Best Local Similarity 54.4%; Score 186; DB 1; Length 60;
 Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 DHPKFCBLPATGSCGVNPRFYTNADHOCLEFYGGCGGANNFTIEGKSTC 57
 DB 2 DRPFCNLAPEBGRGRGHLRIYTNLESNCKKVFYGGCGGANNFTIEGKSTC 57
 RESULT 10
 IYB2_ANESU STANDARD; PRT; 62 AA.
 AC P10280;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protease inhibitor 5 II (SAS II).
 OS Anemonea sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nymphaeae; Actinellidae; Anemonea.
 OX NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE OF 1-59.
 RA Wunderer G., Machleidt W., Fritz H.;
 RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 Anemonea sulcata." ;
 RT Meth. Enzymol. 80:816-820(1981).
 RN [2]
 RA SEQUENCE.
 RP Krebs H.C., Habermann G.G.;
 RT "Isolation and structural determination of a hemolytic active peptide
 from the sea anemone Metridium senile." ;
 RT Naturwissenschaften 74:395-396(1987).
 CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S07451; S07451.
 DR HSSP; P11713; 1SHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Serine protease inhibitor.
 FT DISULFID 5 55
 FT DISULFID 14 38
 FT DISULFID 30 51
 FT ACT SITE 15 16
 FT VARIANT 13 13 A -> R.
 FT VARIANT 16 16 A -> G.
 FT VARIANT 17 17 R -> G.
 FT VARIANT 25 25 S -> L.
 FT VARIANT 28 28 K -> R.
 FT VARIANT 39 39 G -> R.
 SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567B88 CRC64;

Query Match
 Best Local Similarity 53.8%; Score 184; DB 1; Length 62;
 Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

OY 7 CELPAAETGSCKGNVPRFYNNADHQCCKFTYGGCGGNANFKTIEBCKSTC 57
 DB 5 CELPKVGVPCARPRRYNNSSKRCCKFTYGGCGGNANFKTIEBCKKVC 55

RESULT 11

IVBK_DENAN STANDARD; PRT; 57 AA.
 AC P00982;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor K (Dendrotoxin delta-Datx) (Toxin
 DE C1313C3)
 OS Dendroaspis angusticeps (Eastern green mamba).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8618;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81045446; PubMed=7429422;
 RA Joubert F.J., Taljaard N.;
 RT "Snake venoms. The amino acid sequences of two proteinase inhibitor
 RT homologues from Dendroaspis angusticeps venom."
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:661-674(1980).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=88318591; PubMed=2457792;
 RA Benishin C.G., Sorensen R.G., Brown W.E., Krueger B.K.,
 RA Blaustein M.P.;
 RT "Four polypeptide components of green mamba venom selectively block
 RT certain potassium channels in rat brain synaptosomes."
 RL Mol. Pharmacol. 34:152-159(1988).
 CC -1- FUNCTION: This protease inhibitor homolog has very low toxicity.
 CC It blocks voltage-gated potassium channels and facilitate
 CC neurotransmitter release.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) is 15 mg/kg by intravenous injection.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A91691; TIEPVA.
 DR HSSP: P00981; IDTK.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI.
 DR ProDom: PD000222; Kunitz_BPTI.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Toxin; Neurotoxin;
 KW Potassium channel inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SO SEQUENCE 57 AA; 6574 MW; A4070CBB141DB3 CRC64;

Query Match 52.0%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 1.7e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 5 KCELPAAETGSCKGNVPRFYNNADHQCCKFTYGGCGGNANFKTIEBCKSTC 57
 DB 3 KYCKPLRIGPCAKRIPRYNNSSKRCCKFTYGGCGGNANFKTIEBCKRTC 55

RESULT 12

IVBK_DENPO STANDARD; PRT; 57 AA.
 AC P00981;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Venom basic protease inhibitor K (Dendrotoxin K).
 OS Dendroaspis polylepsis polylepsis (Black mamba).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8620;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=77158059; PubMed=857902;
 RT Strydom D.J.;
 RA "Snake venom toxins. The amino acid sequence of toxin Vi2, a
 RT homologue of pancreatic trypsin inhibitor, from Dendroaspis polylepsis
 RT polylepsis (black mamba) venom."
 RL Biochim. Biophys. Acta 491:361-369(1977).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94076347; PubMed=8254670;
 RA Berndt K.D., Guentert P., Wuehrlich K.;
 RT "Nuclear magnetic resonance solution structure of dendrotoxin K from
 RT the venom of Dendroaspis polylepsis polylepsis."
 RL J. Mol. Biol. 234:735-750(1993).
 CC -1- FUNCTION: This protein is much less toxic to mice than is whole
 CC venom. It inhibits trypsin slightly, but chymotrypsin not at all.
 CC It is a highly selective blocker of voltage-gated potassium
 CC channels.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) IS 30 MG/KG BY INTRAVENOUS INJECTION.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PDB: IDTK; 3I-JAN-94.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI.
 DR ProDom: PD000222; Kunitz_BPTI.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
 KW 3D-structure; Potassium channel inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 FT STRAND 18 24
 FT TURN 25 28
 FT STRAND 29 35
 FT STRAND 45 45
 FT HELIX 48 55
 SO SEQUENCE 57 AA; 6566 MW; C30818FB3C41CB87 CRC64;

Query Match 52.0%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 1.7e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 5 KCELPAAETGSCKGNVPRFYNNADHQCCKFTYGGCGGNANFKTIEBCKSTC 57
 DB 3 KYCKPLRIGPCAKRIPRYNNSSKRCCKFTYGGCGGNANFKTIEBCKRTC 55

RESULT 13

CSTI_BOMMO STANDARD; PRT; 55 AA.
 ID CSTI_BOMMO
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyota; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]

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RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Asahi;
RA MEDLINE=99115431; PubMed=9914483;
RT Kuritaka A., Yamazaki M., Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
RT Bombyx mori.";
RL Eur. J. Biochem. 259:120-126(1999).
CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
CC activity by forming a low-dissociation complex with trypsin. May
CC play an important part in regulating proteolytic activity in the
CC silk gland or protecting silk proteins from degradation during
CC histolysis.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
CC gland.
CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
CC middle silk glands during the final stage of larval growth with
CC highest expression before the onset of spinning.
CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC HSSP: P31713; 1SRP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASB.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Developmental protein; Serine protease inhibitor.
KW DISULFID 4 BY SIMILARITY.
FT DISULFID 13 37 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY
FT SEQUENCE 55 AA; 6027 MW; C2739B8B82BB6E59 CRC64;

Query Match 50.3%; Score 172; DB 1; Length 55;
Best Local Similarity 54.9%; Pred. No. 8.5e-14;
Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 7 CELPAETGSCGNVPRFYNDADHOCLEKFIYGGCGGANNFKTIEGKSTC 57
DB 4 CLPFIKTPCKSGSPRAYDSESDKCVBPIYGGCGGANNFKTIEGKSTC 54

RESULT 14
IYBE_DENPO STANDARD; PRT; 59 AA.
ID IYBE_DENPO
AC P00984;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Venom basic protease inhibitor B (Dendrocoxin B).
OS Dendroaspis polylepis polylepis (Black Mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Dendroaspis.
OC NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=78214615; PubMed=666688;
RY Joubert F.J., Strydom D.J.;
RT "Snake venoms. The amino-acid sequence of trypsin inhibitor B of
RT Dendroaspis polylepis polylepis (Black Mamba) venom.";
RL Eur. J. Biochem. 87:191-196(1978).
CC -1- FUNCTION: This protein inhibits trypsin and binds transition metal
CC ions such as copper and cobalt.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: A01215; TIEPD.
DR HSSP: P00981; LDTK.

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DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT_SITE 17 18 REACTIVE BOND (BY SIMILARITY).
FT SEQUENCE 59 AA; 6620 MW; E87BFBECC090276 CRC64;

Query Match 50.3%; Score 172; DB 1; Length 59;
Best Local Similarity 54.5%; Pred. No. 9.1e-14;
Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 3 HPKCELPATGSCGNVPRFYNDADHOCLEKFIYGGCGGANNFKTIEGKSTC 57
DB 3 HTPFCKLPATGSCGNVPRFYNDADHOCLEKFIYGGCGGANNFKTIEGKSTC 57

RESULT 15
TFPI_MACMU STANDARD; PRT; 304 AA.
ID TFPI_MACMU
AC Q28864;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DB associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
DE TFPI OR TFPI1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94375417; PubMed=8089087;
RA Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
RA Yonemura H., Miyamoto S., Funatsu A., Enjoji K., Abumaya T.;
RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
RT factor pathway inhibitor (TFPI): comparison with human TFPI.";
RL J. Biochem. 115:708-714(1994).
CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTIHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S73317; AAB31955.1; -.
DR PIR: JG2264; JG2264.
DR HSSP: P10646; ITRF.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 3.
DR PRINTS: PR00759; BASICPTASB.
DR ProDom: PD000222; Kunitz_BPTI; 3.
DR SMART: SM00131; KU; 3.

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DR PROSITE; PS00280; BPTI KUNITZ 1; 3.
DR PROSITE; PS50279; BPTI KUNITZ 2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL. 1 28 BY SIMILARITY.
FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.
FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1
FT FT (VII (A)/TISSUE FACTOR BINDING SITE).
FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 2
FT FT (FACTOR X(A) BINDING SITE).
FT FT BPTI/KUNITZ INHIBITOR 3.
FT DOMAIN 217 267 BY SIMILARITY.
FT DISULFID 54 104 BY SIMILARITY.
FT DISULFID 63 87 BY SIMILARITY.
FT DISULFID 79 100 BY SIMILARITY.
FT ACT SITE 64 65 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 125 175 BY SIMILARITY.
FT DISULFID 134 158 BY SIMILARITY.
FT DISULFID 150 171 BY SIMILARITY.
FT ACT SITE 135 136 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 217 267 BY SIMILARITY.
FT DISULFID 226 250 BY SIMILARITY.
FT DISULFID 242 263 BY SIMILARITY.
FT ACT SITE 227 228 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FP1628280 CRC64;

Query Match 49.1%; Score 168; DB 1; Length 304;
Best Local Similarity 49.1%; Pred. No. 1.3e-12;
Matches 28; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KDHKFCGLPAETGSCGKAVPRFYADHQCLEKFTYGGCGGANNPKTIEGKSTC 57
DB 119 QEKPDPCFLIEDPDCIGRYITRYFYNNQSKQCRERFKYGGCLGNNMNPETLECKNTC 175

Search completed: January 23, 2004, 10:25:14
Job time : 5.40141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 9.14085 Seconds
(without alignment)
620.725 Million cell updates/sec

Title: US-09-700-179A-8

Sequence: 342 1 KDHPKCELPARTGSCKNV.....CGGNANFKTIEBKSTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	224	65.5	61	1	TIYVTT1
2	212	62.0	57	2	S13846
3	209	61.1	57	1	TINAVC
4	207	60.5	57	1	TIYVVC
5	207	60.5	65	1	TIYIVC
6	202	59.1	62	2	A44180
7	189	55.3	62	2	TIYVZ2
8	186	54.4	60	1	TIYVAV2
9	184	53.8	62	2	S07451
10	178	52.0	57	1	TIYVPA
11	178	52.0	79	1	TIYVPK
12	174	50.3	57	2	A59204
13	172	50.3	57	2	B59399
14	172	50.3	59	1	TIYVED
15	172	50.3	59	2	A59399
16	168	49.1	304	1	JC2264
17	166	48.5	55	2	S30332
18	166	48.5	302	1	TIYVVK
19	165	48.2	110	1	TIYVOR
20	165	48.2	299	2	I46937
21	165	48.2	300	2	S12143
22	164	48.0	58	1	TIYVAK
23	161	47.1	304	1	TIYVVK
24	157	45.9	57	2	S12957
25	156	45.6	396	2	S53325
26	154	45.0	1558	2	C89114
27	154	45.0	2167	2	T34395
28	153	44.7	59	1	VIYVIA
29	152	44.4	249	2	T32060

30	150	43.9	60	1	TIYVVI	venom basic protei
31	150	43.9	235	2	A54951	tissue factor path
32	146	42.7	102	2	A69288	early lactation pr
33	146	42.7	2225	2	T26063	hypothetical prote
34	144	42.1	805	2	T34212	hypothetical prote
35	143	41.8	59	2	S00371	isoprotein G1 -
36	143	41.8	100	1	TIYBO	basic proteinase 1
37	143	41.8	111	2	S41082	amyloid precursor
38	143	41.8	747	2	UH0773	Alzheimer's diseas
39	141	41.2	58	2	S10063	isoprotein G2 -
40	141	41.2	60	2	TIYBOR	serum basic protei
41	141	41.2	751	2	A36989	calcitriol - eas
42	141	41.2	751	2	A49974	beta-amyloid precu
43	141	41.2	763	2	A49321	amyloid beta (A4)
44	140	40.9	57	1	TIYVVB	venom basic protei
45	139	40.6	76	2	S04855	Alzheimer's diseas

ALIGNMENTS

RESULT 1

TIYVTT1
venom basic proteinase inhibitor I - western sand viper

N/Alternate names: venom trypsin inhibitor I
C/Species: Vipera ammodytes ammodytes (western sand viper)

C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996

C/Accession: A01222

R/Rittonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 748, 429-435, 1993

A/Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.

A/Reference number: A01222; PMID:84053385; PMID:6639951

A/Accession: A01222

A/Molecule type: protein

A/Residues: 1-61 <RIT>

C/Comment: This protein inhibits trypsin and kallikrein.

C/Suprafamily: basic proteinase inhibitor, animal Kunitz-type proteinase inhibitor hom

C/Keywords: pyroglutamic acid; serine proteinase inhibitor; venom

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

F/7-57,16-40,32-53/Disulfide bonds: #status predicted

F/7/Inhibitory site: Lys (trypsin) #status predicted

Query Match 65.5%; Score 224; DB 1; Length 61;

Best local similarity 62.7%; Pred. No. 1,5e-19;

Matches 37; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Db 1 KDHPKCELPARTGSCKNVPRFYVADHHCILKFTYGGCGGNANFKTIEBKSTCA 59

1 QDHPKCELPADPGRCCKAHIPRYVDSASNKCKFTYGGCGGNANFKTIEBKSTCA 59

RESULT 2

S13846
venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)

C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000

R/Shafigat, U.; Begal, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.
Eur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja) venom K

A/Reference number: S13846; PMID:91099304; PMID:1702708

A/Accession: S13846

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SHA>

C/Suprafamily: basic proteinase inhibitor, animal Kunitz-type proteinase inhibitor hom

C/Keywords: serine proteinase inhibitor; venom

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 62.0%; Score 212; DB 2; Length 57;

Best local similarity 66.7%; Pred. No. 3.6e-18;

Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 4 PKFCPLPAETGCKGNVPRYPYNADHQC LFIYGGCGGNANNEKTEIEGKSTC 57
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 2 PGFCPLPAKGLCKAHKPAFYNNKDSHCQKFIYGGCGGNANRFRITIDCNRTC 55

RESULT 3

venom basic proteinase inhibitor II - Cape cobra
 C.Species: Naja nivea (Cape cobra)
 C.Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C.Accession: A01217
 R.Hokema, Y., Iwanaga, S., Tateuchi, T., Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A.Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitors
 o acid sequences of two of them.
 o Reference number: A91942; MUID: 76237547; PMID: 950337
 A.Accession: A01217
 A.Molecule type: protein
 A.Residues: 1-57 <HOK>
 C.Comment: The activity of this inhibitor is probably similar to that of bovine basic pr
 C.Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C.Keywords: serine proteinase inhibitor; venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Dissulfide bonds: #status predicted

Query Match	61.1%	Score 209;	DB 1;	Length 57;
Best Local Similarity	66.7%	Pred. No. 8.2e-18;		
Matches 36; Conservative	5;	Mismatches 13;	Indels 0;	Gaps 0

```
Oy      4 PKFCFLPAETGSCKGNVPRFYNNADHQCLKEIYGGCGGANNFKEITBEGSTC 57
         |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      2 PRFCELP AETGLCKARIRSFHNRAQCLFIYGGCGGANRPFKTIDECRTCC 55
```

RESULT 4

venom basic proteinase inhibitor II - ringhals
C.Species: Hemachatus haemachatus, Gepdon haemachatus (ringhals)
C.Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C.Accession: A01216
R.Hokama, Y.; Iwanaga, S.; Tateuki, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A.Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitors
o acid sequences of two of them.
A.Reference number: A91942; MUID:76237547; PMID:950337
A.Accession: A01216
A.Molecule type: protein
A.Residues: 1-57 <HOK>
C.Comment: The activity of this inhibitor is similar to that of bovine basic protease inhibitor
C.Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology
C.Keyword: serine proteinase inhibitor; venom
F.5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F.5-55, 14-38, 30-51/Dsulfide bonds: #catus predicted

Query Match	60.5%	Score 207;	DB 1;	Length 57;
Best Local Similarity	66.7%	Pred. No. 1.4e-17;		
Matches 36;	Conservative	5;	Mismatches 13;	Indels 0;
			Gaps	0

Qy 4 PKFCELPAAETGSCKGNVPRFYNNADHQCIFITYGGCGGNANPKTIBEGKSTC 5
| | | | | : | | | | | : | | | | | : | |
Db 2 PDFCELPAAETGCLCKAYIRSFHYNLAAQCQCFITYGGCGGNANRFKTIIDECARTC 5

RESULT

venom basic proteinase inhibitor III - sand viper
 Maltetrans names: venom chymotrypsin inhibitor
 C/Species: Vipera ammodytes (sand viper)
 C/Date: 17-May-1985 #sequence revision 17-May-1985 #text change 16-Aug-1996
 C/Accession: A01123
 R/Rittona, A.; Meloun, B.; Gubensek, F.
 Biochim. Biophys. Acta 746, 138-145, 1983

A;Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor
A;Reference number: A01223

A;Molecule type: protein
A;Residues: 1-65 <RIT>

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor no
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal kunitz-type proteinase inhibitor homology
F:7-57,16-40,32-53/Disulfide bonds: #acrtatus predicted
F:17/Inhibitory site: Ven (chymotrypsin) #acrtatus predicted

Query Match	60.5%;	Score 207;	DB 1;	Length 65;
Best Local Similarity	61.0%;	Pred. NO. 1.6e-17;		
Matches 36;	Conservative 7;	Mismatches 16;	Indels 0;	Gaps 0;

Qy 1 KDHPKCELPATGSCCKGNVPRFYNNADHHQCLKPIYGGCGGNANFNFTIEEGSTCAA 59

Db 1 KDRPKFCFLPADBGRCLAYMPRPFYNNPASKCKEPIYGGCGGNANFNFTYDECHTTCVA 59

RESULT 6

taicetoxin serine proteinase inhibitor component - Australian taipan
C/Species: *Oxyuranus scutellatus scutellatus* (Australian taipan)
C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C/Accession: A44180
R/Possant, L.D.; Martin, B.M.; Yatani, A.; Mochica-Morales, J.; Zamudio, F.Z.; Gurrola-
Toxicon 30, 1343-1364, 1992
A/Title: Isolation and physiological characterization of taicetoxin, a complex toxin v
A/Reference number: A44180; PMID:1455334

A;Accession: A1120
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <POS>

A:Experimental source: subsp. scutellatus, venom
A-Note: sequence extracted from NCBI backbone (NCBI:P.122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology
C:Keywords: serine proteinase inhibitor
P:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match	59.1%	Score 202	DB 2	Length 62
Best Local Similarity	61.4%	Pred. No.	6e-17	
Matches 35	Conservative 4	Mismatches 18	Indels 0	Gaps 0

Oy

1	KDHPKFCCLPAETGSCCKGNVPRFYNNADHHQCLKRIYGGCGGNANNEKTIEGSKTC	57
:	: : : :	:
:	: : : :	:

Dd

1	KDRPKFCHLPPKPGPCRAIIPRFYYNPHSQCEKEFIYGSGGNANNEKTPDECNITC	57
---	--	----

RESULT

venom basic proteinase inhibitor - leaf-nosed viper
 N:Alternate names: trypsin inhibitor (kunitz-type)
 C:Species: Eristocophis maculatus (leaf-nosed viper)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S19327
 R:Sididigt, A.R.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 294, 141-143, 1991
 A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from *Le*
 A:Reference number: S19327, PMID:92077130, PMID:1743283
 A:Accession: S19327
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-62 <SID>
 C:superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor. hom
 C:keywords: serine proteinase inhibitor; venom
 P:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

Query Match	55.3%	Score 189,	DB 2,	Length 62;
Best Local Similarity	59.3%	Pred. No. 2e-15,		
Matches 33; Conservative	7;	Mismatches 15,	Indels 0,	Gaps 0.

QY 6 PCBLPAETGCKGNVPRFYNNADHQCCKFYGGCGNANFKTIEGKSTCAA 59

Db 1 FGVLPDDPGVCKAIPFRYYNPASNCKNPFYGGCGGANNFETRAECRHTCVA 54

RESULT 8

TIIEPV2

venom basic proteinase inhibitor II - Russell's viper

C/Species: Viper russelli (Russell's viper)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C/Accession: A01221

R./Accession: A01221

J./Accession: A01221

A./Accession: A01221

A./Accession: A01221

A./Accession: A01221

A./Accession: A01221

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A./Accession: A01221

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 28.4613 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179A-8
Sequence: 342
1 KDHPCFCELPATGSCCKGNV.....CGGNANNKTIIEGKSTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

- 1: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
- 2: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
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- 24: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	342	100.0	59	21 AA15141 Txln 4 Plasmin inh
2	342	100.0	83	21 AA15148 Proform of Txln 4
3	256	74.9	59	21 AA15140 Txln 3 Plasmin inh
4	256	74.9	83	21 AA15147 Proform of Txln 3
5	225	65.8	59	21 AA15138 Txln 1 Plasmin inh
6	225	65.8	83	21 AA15145 Proform of Txln 1
7	218	63.7	60	21 AA15153 Plasmin inhibitor
8	217	63.5	59	21 AA15139 Txln 2 Plasmin inh
9	217	63.5	83	21 AA15146 Proform of Txln 2

10	211	61.7	58	17 AA899146
11	201	58.8	59	21 AA15142
12	201	58.8	83	21 AA15149
13	193	56.4	60	21 AA15154
14	192	56.1	59	21 AA15143
15	192	56.1	83	21 AA15150
16	192	56.1	83	21 AA62525
17	178	52.0	57	15 AA81911
18	170	50.3	58	16 AA878542
19	168	49.1	58	16 AA81915
20	168	49.1	304	14 AA842309
21	166	48.5	58	16 AA81892
22	166	48.5	58	17 AA899197
23	166	48.5	302	14 AA835001
24	166	48.5	302	17 AA888513
25	165	48.2	58	17 AA899195
26	164	48.0	58	14 AA839800
27	164	48.0	111	14 AA839807
28	162	47.4	58	17 AA899194
29	162	47.4	161	17 AA800017
30	162	47.4	291	24 ABR48476
31	162	47.4	291	24 ABR48478
32	161	47.1	71	13 AA837399
33	161	47.1	110	12 AA81145
34	161	47.1	111	14 AA839804
35	161	47.1	160	13 AA823800
36	161	47.1	183	12 AA81146
37	161	47.1	225	22 AA002971
38	161	47.1	256	12 AA81169
39	161	47.1	261	12 AA81171
40	161	47.1	262	12 AA81172
41	161	47.1	265	12 AA81170
42	161	47.1	276	17 AA892265
43	161	47.1	276	17 AA892012
44	161	47.1	276	18 AA810311
45	161	47.1	276	19 AA861535

ALIGNMENTS

RESULT 1
ID AA15141 standard; Protein; 59 AA.

AA15141;
07-FEB-2000 (first entry)

Txln 4 Plasmin inhibitor protein.

Textilinin protein; Txln 4; plasmin inhibitor; single stage inhibitor; Australian brown snake; conserved cysteine residue; stability; control; haematopoietic; cytosolic activity; specificity; inhibitory efficiency; fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme; fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent; reduced propensity; thrombosis.

Pseudonaja textilis textilis.

WO9958569-A1.
18-NOV-1999.

07-MAY-1999; 99WO-AU00343.
11-MAY-1998; 98AU-0003450.

(UYOU) UNIV QUEENSLAND.
(MABI-) NAT INST BIOLOGICAL STANDARDS & CO.
(MASC/) MASC P P.
(LAVI/) LAVIN M F.
(GAFF/) GAFFNEY P J.

Aporofin-like Kun
Txln 5 Plasmin inh
Proform of Txln 5
Plasmin inhibitor
Txln 6 Plasmin inh
Proform of Txln 6
Protease-inhibitor
Kallikrein inhibit
Human Lact-K2 deri
Lacti gene product.
Kallikrein inhibit
Genetically engine
Lacti. Rattus rat
Lipoprotein-associ
Genetically engine
Kunitz-type protea
Synthetic yeast le
Genetically engine
TFPI chimeric prot
Human Tifepinix.
Human Tifepinix-A5
Lacti fragment 1 -
Synthetic yeast le
Lacti fragment 1 -
Ser-(Glu15-Thr161)
Angiotensin conver
Ser-(Asp1-Thr255)-E
Ser-(Asp1-Glu245)-
Ser-(Asp1-Ser248)-
Ser-(Asp1-Ile253)-
TFPI mutein, Lys36
TFPI mutein K36R.
Recombinant non-gl
Human tissue facto


```

XX  Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
PI  WPI: 2000-039073/03.
XX  N-PSDB; AAZ29020.
DR  Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX  agents -
XX  Claim 8d; Page 69; 112pp; English.
XX
XX  The present sequence is the Textillin protein, Txln 4, that is a
XX  single stage competitive inhibitor of plasmin. It is isolated from the
XX  Australian brown snake, Pseudonaja textilis textilis. It has six
XX  conserved cysteine residues, that endow them great stability. This
XX  sequence has haematopoietic and cytostatic activity. Txln has high
XX  specificity for plasmin and low inhibitory efficiency, that can
XX  transiently affect the delicate balance between enzymes and inhibitors
XX  of the fibrinolytic system, controlling the fluidity of blood. The
XX  plasmin inhibitors are useful for alleviating blood loss, following
XX  major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX  anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX  propensity to cause thrombosis.
XX
XX  Sequence 59 AA;
SQ
XX
XX  Query Match 100.0%; Score 342; DB 21; Length 59;
XX  Best Local Similarity 100.0%; Pred. No. 2.3e-35;
XX  Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 KDHPKFCBLPAPGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 59
XX
XX  RESULT 2
XX  ID AAY15148 standard; Protein; 83 AA.
XX  AC AAY15148;
XX  DT 07-FEB-2000 (first entry)
XX  DE Proform of Txln 4 protein.
XX
XX  Textillin proform; Txln 4; plasmin inhibitor; single stage inhibitor;
XX  Australian brown snake; conserved cysteine residue; stability; control;
XX  haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX  fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX  fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX  reduced propensity; thrombosis.
XX
XX  Pseudonaja textilis textilis.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..24
XX  Protein 25..83
XX  /label= Txln-4_protein
XX  /note= "Textillin-4"
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XX  WO9958569-A1.
XX  18-NOV-1999.
XX
XX  07-MAY-1999; 99WO-AU00343.
XX
XX  11-MAY-1998; 98AU-0003450.
XX
XX  (UYOU ) UNIV QUEENSLAND.
XX  (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX  (MASC/) MASI P P.
XX  (LAVI/) LAVIN M F.

```

```

PA  (GAFF/) GAFFNEY P J.
XX  Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
PI  WPI: 2000-039073/03.
XX  N-PSDB; AAZ29027.
DR  Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX  agents -
XX  Claim 40d; Page 72; 112pp; English.
XX
XX  The present sequence is the proform of the Textillin protein, Txln 4,
XX  that is a single stage competitive inhibitor of plasmin. It is isolated
XX  from the Australian brown snake, Pseudonaja textilis textilis. It has
XX  six conserved cysteine residues, that endow them great stability. This
XX  sequence has haematopoietic and cytostatic activity. Txln has high
XX  specificity for plasmin and low inhibitory efficiency, that can
XX  transiently affect the delicate balance between enzymes and inhibitors
XX  of the fibrinolytic system, controlling the fluidity of blood. The
XX  plasmin inhibitors are useful for alleviating blood loss, following
XX  major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX  anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX  propensity to cause thrombosis.
XX
XX  Sequence 83 AA;
SQ
XX
XX  Query Match 100.0%; Score 342; DB 21; Length 83;
XX  Best Local Similarity 100.0%; Pred. No. 3.3e-35;
XX  Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 KDHPKFCBLPAPGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 59
DB 25 KDHPKFCBLPAPGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 83
XX
XX  RESULT 3
XX  ID AAY15140 standard; Protein; 59 AA.
XX  AC AAY15140;
XX  DT 07-FEB-2000 (first entry)
XX  DE Txln 3 Plasmin inhibitor protein.
XX
XX  Textillin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
XX  Australian brown snake; conserved cysteine residue; stability; control;
XX  haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX  fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX  fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX  reduced propensity; thrombosis.
XX
XX  Pseudonaja textilis textilis.
XX
XX  WO9958569-A1.
XX  18-NOV-1999.
XX
XX  07-MAY-1999; 99WO-AU00343.
XX
XX  11-MAY-1998; 98AU-0003450.
XX
XX  (UYOU ) UNIV QUEENSLAND.
XX  (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX  (MASC/) MASI P P.
XX  (LAVI/) LAVIN M F.
XX  (GAFF/) GAFFNEY P J.
XX
XX  Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
PI  WPI: 2000-039073/03.
XX  N-PSDB; AAZ29019.

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XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 8c; Page 69; 112pp; English.
 CC The present sequence is the Textillinin protein, Txln 3, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 XX
 Query Match 74.9%; Score 256; DB 21; Length 59;
 Best Local Similarity 71.2%; Pred. No. 1.4e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 KDHPKCELPARTGSCKGNVPRFYNNADHOCLEKRIYGGCGGANNPFTIEBGSCTCA 59
 Db 1 KDRPNFCKLPARTGRCNAKIRPFYNNPRHOCIEFLYGGCGGANNPFTIEBGSCTCA 59
 RESULT 4
 AAY15147
 ID AAY15147 standard; Protein; 83 AA.
 AC AAY15147;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Proform of Txln 3 protein.
 XX
 KW Textillinin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Leader_peptide
 FT /label= Txln-3 protein
 FT /note= "Textillinin-3"
 XX
 PN W09958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavlin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI, 2000-039073/03.
 DR

DR N-PSDB; AA229026.
 XX
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 40c; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textillinin protein, Txln 3,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 83 AA;
 XX
 Query Match 74.9%; Score 256; DB 21; Length 83;
 Best Local Similarity 71.2%; Pred. No. 2e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 KDHPKCELPARTGSCKGNVPRFYNNADHOCLEKRIYGGCGGANNPFTIEBGSCTCA 59
 Db 25 KDRPNFCKLPARTGRCNAKIRPFYNNPRHOCIEFLYGGCGGANNPFTIEBGSCTCA 83
 RESULT 5
 AAY15138
 ID AAY15138 standard; Protein; 59 AA.
 AC AAY15138;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Txln 1 Plasmin inhibitor protein.
 XX
 KW Textillinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; homology; specificity; Apoptin;
 KW falcotoxin-associated plasmin inhibitor; Tac; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Leader_peptide
 FT /label= Txln-3 protein
 FT /note= "Textillinin-3"
 XX
 PN W09958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavlin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI, 2000-039073/03.
 DR N-PSDB; AA229017.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX

PS Claim 8a; Page 68; 112pp; English.

CC The present sequence is the Textillin protein, Txln 1, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
 CC 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.

XX Sequence 59 AA;

SQ Query Match 65.8%; Score 225; DB 21; Length 59;

Best Local Similarity 67.8%; Pred. No. 1e-20; Mismatches 14; Indels 0; Gaps 0;

Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

1 KDHPKCELPATGSCGKGVPRFYVADHHCCKFTYGGCGGNANFKTIEGKSTCA 59
 1 KDRPDCFLPADTGCRVAFPSFYVADHHCCKFTYGGCGGNANFKTIEGKSTCA 59

RESULT 6

ID AAY15145

AAV15145 standard; Protein; 83 AA.

AC AAY15145;
 DT 07-FEB-2000 (first entry)
 DB Perform of Txln 1 protein.

XX Textillin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 XX haematopoietic; cytostatic activity; homology; specificity; control;
 XX Talcotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

OS Pseudonaja textilis textilis.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader_peptide
 FT Protein 25..83
 FT /label= Txln-1 protein
 FT /note= "Textillin-1"

XX WO958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFNEY P J.

XX Masei PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV;
 DR MPI; 2000-039073/03.
 DR N-PSDB; AA229024.
 XX

PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -

PS Claim 40a; Page 71; 112pp; English.

XX The present sequence is the proform of the Textillin protein, Txln 1,
 XX that is a single stage competitive inhibitor of plasmin. It is isolated
 XX from the Australian brown snake, Pseudonaja textilis textilis. It has
 XX six conserved cysteine residues, that endow them great stability. This
 XX sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
 XX 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 XX (TAC), respectively. Txln has high specificity for plasmin and low
 XX inhibitory efficiency, that can transiently affect the delicate balance
 XX between enzymes and inhibitors of the fibrinolytic system, controlling
 XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
 XX blood loss, following major surgery or trauma. Conjugates of the plasmin
 XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 XX They have reduced propensity to cause thrombosis.

XX Sequence 83 AA;

SQ Query Match 65.8%; Score 225; DB 21; Length 83;

Best Local Similarity 67.8%; Pred. No. 1.5e-20; Mismatches 14; Indels 0; Gaps 0;

Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

1 KDHPKCELPATGSCGKGVPRFYVADHHCCKFTYGGCGGNANFKTIEGKSTCA 59
 25 KDRPDCFLPADTGCRVAFPSFYVADHHCCKFTYGGCGGNANFKTIEGKSTCA 83

RESULT 7

ID AAY15153

AAV15153 standard; Protein; 60 AA.

AC AAY15153;
 DT 07-FEB-2000 (first entry)
 DB Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.

XX Textillin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 XX haematopoietic; cytostatic activity; homology; specificity; enzyme;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX inhibitory efficiency; reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX Key Location/Qualifiers
 FH Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 47
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"

XX WO958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFNEY P J.

XX Masei PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV;
 DR MPI; 2000-039073/03.
 DR N-PSDB; AA229024.
 XX

DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ29047.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Disclousure; Fig 6; 112pp; English.
 CC The present amino acid sequence is the Txln 1, Textillin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 60 AA;
 Query Match 63.7%; Score 218; DB 21; Length 60;
 Best Local Similarity 64.4%; Pred. No. 8e-20; Mismatches 15; Indels 0; Gaps 0;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 Oy 1 KDHKPCFELPAETSCGKNVRFYYNADHHQCLKEFYGGCGGANNFKTIEGKSTCA 59
 Db 2 KDRPDPFCELPADTPCVRPRPSFYTNDEKCKLEFYGGCGGANNFKTIEGKSTCS 60
 RESULT 8
 ID AAY15139 standard; Protein; 59 AA.
 AC AAY15139;
 XX
 XX 07-FEB-2000 (first entry)
 DE Txln 2 Plasmin inhibitor protein.
 XX
 XX Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; homology; specificity; Aprotinin;
 KM Talicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 XX W09958569-A1.
 PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F J.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29018.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Claim 8b; Page 69; 112pp; English.

XX
 CC The present sequence is the Textillin protein, Txln 2 that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 2 has 43% and
 CC 55% homology with Aprotinin and Talicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 Query Match 63.5%; Score 217; DB 21; Length 59;
 Best Local Similarity 64.4%; Pred. No. 1.1e-19; Mismatches 15; Indels 0; Gaps 0;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 Oy 1 KDHKPCFELPAETSCGKNVRFYYNADHHQCLKEFYGGCGGANNFKTIEGKSTCA 59
 Db 1 KDRPDPFCELPADTPCVRPRPSFYTNDEKCKLEFYGGCGGANNFKTIEGKSTCA 59
 RESULT 9
 ID AAY15146 standard; Protein; 83 AA.
 AC AAY15146;
 XX
 XX 07-FEB-2000 (first entry)
 DE Proform of Txln 2 protein.
 XX
 XX Textillin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KM haematopoietic; cytosolic activity; homology; specificity; control;
 KM Talicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader peptide
 FT 25..83
 FT /label= Txln-2 protein
 FT /note= "Textillin-2"
 XX
 XX W09958569-A1.
 PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F J.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29025.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX

PT agents -
 XX Claim 40b; Page 71; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillin protein, Txln 2,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 2 has 43% and
 CC 55% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAc), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX
 SQ Sequence 83 AA;
 Query Match 63.5%; Score 217; DB 21; Length 83;
 Best Local Similarity 64.4%; Pred. No. 1.5e-19;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 QY 1 KDHPFCELPARTGCKGNVPRFYNNADRHQCLKFTYGGCGGNANFKTIEEGKSTCA 59
 DB 25 KDRPELCBLPPTGTCRVAPPSFYNNPDBQKCLFITYGCGGNANFKTIEEGKSTCA 83
 RESULT 10
 AAR9146 AAR9146 standard; protein; 58 AA.
 XX AAR9146;
 AC
 XX 12-FEB-1997 (first entry)
 DT
 XX Aprotinin-like Kunitz domain.
 DE
 XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha1 antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.
 KM
 XX Synthetic.
 OS
 XX MO9620278-A2.
 PN
 XX 04-JUL-1996.
 PD
 XX 15-DEC-1995; 95WO-US16349.
 PF
 XX 16-DEC-1994; 94US-0358160.
 PR
 XX (PROT-) PROTEIN ENG CORP.
 PA
 XX Guerman SK, Kent RB, Ladner RC, Ley AC, Markland W;
 PI Roberts BL;
 PT WPI; 1996-321851/32.
 DR
 XX New engineered inhibitors of human neutrophil elastase - contd.
 PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
 PT other respiratory disorders
 XX
 XX Example 23; Page 47; 105pp; English.
 PS Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the
 CC elimination of pathogens and the restructuring of connective tissue.
 CC In cases of reduction of the circulating alpha-1-protease inhibitor
 CC (API or alpha1 antitrypsin), or the inactivation of API by oxidation
 CC (smokers emphysema), extensive destruction of the lung tissue may

CC result from uncontrolled elastolytic activity of human neutrophil
 CC elastase. Other respiratory disorders such as cystic fibrosis are
 CC thought to be caused by human neutrophil elastase release by
 CC neutrophils. The genetically engineered human derived Kunitz
 CC domains can be used to treat such respiratory disorders. See
 CC AAR9146-R39211.
 XX
 SQ Sequence 58 AA;
 Query Match 61.7%; Score 211; DB 17; Length 58;
 Best Local Similarity 68.5%; Pred. No. 5.8e-19;
 Matches 37; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 4 PRCFELPARYGCKGNVPRFYNNADRHQCLKFTYGGCGGNANFKTIEEGKSTC 57
 DB 2 PFCFLPARYGCRAMIRPFYNNASGCKEPIFYGGCGGNANFKTIEEGKSTC 55
 RESULT 11
 AAY15142
 ID AAY15142 standard; protein; 59 AA.
 XX AAY15142;
 AC
 XX 07-FEB-2000 (first entry)
 DT
 XX Txln 5 Plasmin inhibitor protein.
 DE
 XX Textillin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 KM
 XX Pseudonaja textilis textilis.
 OS
 XX WO958569-A1.
 PN
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-AU00343.
 PF
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 XX
 PI Masci PP, Lavlin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AA229021.
 DR
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PT
 XX Claim 8e; Page 69; 112pp; English.
 PS The present sequence is the Textillin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX SQ Sequence 59 AA;
 Query Match 58.8%; Score 201; DB 21; Length 59;
 Best Local Similarity 61.0%; Pred. No. 1.1e-17;
 Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFTIEBKGSTCA 59
 Db 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFTIEBKGSTCA 59

RESULT 12
 AAY15149
 ID AAY15149 standard; Protein; 83 AA.
 AC AAY15149;
 DT 07-FEB-2000 (first entry)
 DE Protein of Txln 5 protein.
 XX Textilin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Leader_peptide
 FT /label= Txln-5 protein
 FT /note= "Textilin-5"
 XX
 PN WO9958569-A1.
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFN/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 DR WPI: 2000-039073/03.
 DR N-PSDB; AAZ29028.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 40e; Page 72; 112pp; English.
 XX
 CC The present sequence is the proform of the Textilin protein, Txln 5,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced

CC propensity to cause thrombosis.
 XX SQ Sequence 83 AA;
 Query Match 58.8%; Score 201; DB 21; Length 83;
 Best Local Similarity 61.0%; Pred. No. 1.6e-17;
 Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFTIEBKGSTCA 59
 Db 25 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFTIEBKGSTCA 83

RESULT 13
 AAY15154
 ID AAY15154 standard; Protein; 60 AA.
 AC AAY15154;
 DT 07-FEB-2000 (first entry)
 DE Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
 XX Textilin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; homology; enzyme;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW inhibitory efficiency; reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 24 /note= "encoded by TTG"
 FT Misc-difference 45 /note= "encoded by GAT"
 FT Misc-difference 49 /note= "encoded by ATG"
 FT Misc-difference 59 /note= "encoded by CGN"
 FT
 PN WO9958569-A1.
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFN/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 DR WPI: 2000-039073/03.
 DR N-PSDB; AAZ29048.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Disclosure; Fig 7; 112pp; English.
 XX
 CC The present amino acid sequence is the Txln 2, Textilin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for

Query Match 56.1%; Score 192; DB 21; Length 83;
 Best Local Similarity 57.6%; Pred. No. 2.1e-16;
 Matches 34; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 Oy 1 KDHKPCFCELPAPETGSCGNVPRFYTNADHOCLEKFIYGGCGGANNPKTIERGKSTCA 59
 Db 25 KDRPKFCELPADIGFWDDFTGAFHYSPREHECIEPIYGGCKGNANFNFTOEOCESTCA 83

Search completed: January 23, 2004, 10:24:35
 Job time : 28.4613 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 9.14085 Seconds
(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179A-2.

Perfect score: 341

Sequence: 1 KDRDPFCELPADTGPCRVRF.....CEGNANPFITKECESTCA 59

Scoring table:

BIOSUM62

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	63.6	62	2	A44180
2	214	62.8	65	1	TIVIVC
3	204	59.8	62	2	S07451
4	201	58.9	57	1	TINJVC
5	201	58.9	61	1	TIVITL
6	198	58.1	57	1	TIRIV2
7	195	57.2	62	2	S19327
8	194	56.9	57	2	S13846
9	189	55.4	110	1	TITROR
10	188	55.1	58	1	TIRABK
11	179	52.5	57	2	B59399
12	179	52.5	59	1	TIRPED
13	179	52.5	59	2	A53399
14	178	52.2	60	1	TIVRV2
15	169	49.6	57	1	TIRPVA
16	169	49.6	302	1	TIRTKG
17	169	49.6	396	2	S53325
18	168	49.3	79	1	TIRPVK
19	168	49.3	304	1	UC2264
20	167	49.0	57	2	A59204
21	165	48.4	57	2	TIRPBP
22	165	48.4	235	2	A54951
23	165	48.4	299	2	I46937
24	165	48.4	300	2	S12143
25	163	47.8	304	2	UG0185
26	161	47.2	304	2	TIRHKG
27	160	46.9	3176	1	CGH03A
28	158	46.3	59	2	S00371
29	156	45.7	58	2	S10063

30	156	45.7	100	1	TIBO	basic proteinase i
31	155	45.5	122	1	A55115	uterine plasmin/tr
32	154	45.2	100	1	TIBOSP	spleen basic prote
33	154	45.2	747	2	JH0773	Alzheimer's diseas
34	153	44.9	57	1	TIRPVB	venom basic protei
35	152	44.6	60	1	TIBOR	serum basic protei
36	152	44.6	76	2	S04855	Alzheimer's diseas
37	152	44.6	100	2	A32282	Alzheimer's diseas
38	150	44.0	76	2	S03607	Alzheimer's diseas
39	150	44.0	76	2	S06678	Alzheimer's diseas
40	150	44.0	111	2	S41082	amyloid precursor
41	150	44.0	484	4	A32761	hypothetical Alzhe
42	150	44.0	770	1	ORH044	Alzheimer's diseas
43	150	44.0	2225	2	T26063	hypothetical prote
44	149	43.7	55	2	S30332	proteinase inhibit
45	149	43.7	751	2	A49974	beta-amyloid precu

ALIGNMENTS

RESULT 1
A44180
taicatoxin serine proteinase inhibitor component - Australian taipan
C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #ext_change 07-Feb-1997
C:Accession: A44180
R:Posami, L.D.; Martin, B.M.; Yatani, A.; Mochizuki-Morales, J.; Zamudio, F.Z.; Guirrola, R.;
Toxicon 30, 1343-1364, 1992
A>Title: Isolation and physiological characterization of taicatoxin, a complex toxin w:
A:Reference number: A44180; PMID:1485334
A:Accession: A44180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Experimental source: subsp. scutellatus, venom
A>Note: sequence extracted from NCBI backbone (NCBIP:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
C:Keywords: serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 63.6%; Score 217; DB 2; Length 62;
Matches 36; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 KDRDPFCELPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANPFITKECESTC 57
DB 1 KDRPFCELPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANPFITKECESTC 57

RESULT 2

TIVIVC
venom basic proteinase inhibitor III - sand viper
N:Alternate names: Venom chymotrypsin inhibitor
C:Species: Viper a ammodytes (sand viper)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #ext_change 16-Aug-1996
C:Accession: A01223
R:Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A>Title: The primary structure Of Viper a ammodytes venom chymotrypsin inhibitor.
A:Reference number: A01223
A:Accession: A01223
A:Molecule type: protein
A:Residues: 1-65 <NT>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:7-57,16-40,32-53/Diulfide bonds: #status predicted
F:17/inhibitory site: Denu (chymotrypsin) #status predicted

Query Match
Best Local Similarity 62.8%; Score 214; DB 1; Length 65;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTCA 59
 Db 1 RDRPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTCA 59

RESULT 3

S07451
 C:Species: Anemone sulcata (snake-locks sea anemone)
 C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C:Accession: S07451; B27222
 R:Munderer, G.; Machleidt, W.; Fritz, H.
 Meth. Enzymol. 80, 816-820, 1981
 A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemone
 A:Reference number: S07451
 A:Accession: S07451

A:Molecule type: protein
 A:Residues: 1-59 <WGN>
 A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
 R:Krebs, H.C.; Habermehl, G.G.
 Naturwissenschaften 74, 395-396, 1987
 A:Title: Isolierung und strukturelle Aufklärung eines haemolytisch aktiven Peptids aus der
 A:Reference number: A94700
 A:Accession: B27222

A:Molecule type: protein
 A:Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'ZZ', '51', 'Z', '53-62' <KRB>
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 59.8%; Score 204; DB 2; Length 62;
 Best Local Similarity 66.7%; Pred. No. 2.7e-16;
 Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTC 57
 Db 5 CELPKVVGCPARPRPSPFYNNSSSKCEKFIYGGCGGNANNFITKECEKTC 55

RESULT 4

TINJVC
 venom basic proteinase inhibitor II - Cape cobra
 C:Species: Naja nivea (Cape cobra)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01217
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01217

A:Molecule type: protein
 A:Residues: 1-57 <HOK>
 C:Comment: The activity of this inhibitor is probably similar to that of bovine basic pr
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor; venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 58.9%; Score 201; DB 1; Length 57;
 Best Local Similarity 63.6%; Pred. No. 5.4e-16;
 Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 3 RDPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTC 57
 Db 1 RRPFCPLPATGTGCKARIRSFHYNNRAQQCLAEFIYGGCGGNANRFKTIDECRTTC 55

RESULT 5

TIVITI
 venom basic proteinase inhibitor I - western sand viper
 N:Alternate names: venom trypsin inhibitor I

C:Species: Viper a ammodytes ammodytes (western sand viper)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
 C:Accession: A01222
 R:Rittonja, A.; Meloun, B.; Gubensek, F.
 Biochim. Biophys. Acta 748, 429-435, 1983
 A:Title: The primary structure of Viper a ammodytes venom trypsin inhibitor I.
 A:Reference number: A01222; MUID:84053385; PMID:6639951
 A:Accession: A01222

A:Molecule type: protein
 A:Residues: 1-61 <RTV>
 C:Comment: This protein inhibits trypsin and kallikrein.
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
 C:Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
 F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:7-57,16-40,32-53/Disulfide bonds: #status predicted
 F:17/inhibitory site: Lys (trypsin) #status predicted

Query Match 58.9%; Score 201; DB 1; Length 61;
 Best Local Similarity 57.6%; Pred. No. 5.8e-16;
 Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTCA 59
 Db 1 QDRPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTCA 59

RESULT 6

TIRIV2
 venom basic proteinase inhibitor II - ringhals
 C:Species: Hemachatus haemachatus, Sepeodon haemachatus (ringhals)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01216
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibit
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01216

A:Molecule type: protein
 A:Residues: 1-57 <HOK>
 C:Comment: The activity of this inhibitor is similar to that of bovine basic protease
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
 C:Keywords: serine proteinase inhibitor; venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 58.1%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 1.2e-15;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 3 RDPFCPLPADTGPCRVPRPSPFYNNPDEKCLAEFIYGGCEGNANNFITKECESTC 57
 Db 1 RDPFCPLPATGTGCKAVIRSFHYNNLAQQCLAEFIYGGCGGNANRFKTIDECRTTC 55

RESULT 7

S19327
 venom basic proteinase inhibitor - leaf-nosed viper
 N:Alternate names: trypsin inhibitor (Kunitz-type)
 C:Species: Eristocophis macramoni (leaf-nosed viper)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S19327
 R:Sididqi, A.R.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 294, 141-143, 1991
 A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Lea
 A:Reference number: S19327; MUID:92077130; PMID:1743283
 A:Accession: S19327

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-62 <SID>
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
 C:Keywords: serine proteinase inhibitor; venom

F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 57.2%; Score 195; DB 2; Length 62;
Best Local Similarity 61.1%; Pred. No. 2.8e-15;
Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 6 FCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTCA 59
Db 1 FCVLPDGGVCKAHIPRYNNPASKCKNFYIGGCGGNANFTTKECHTCA 54

RESULT 8

venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)
C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #ext_change 17-Mar-2000

C/Accession: S13846
R:Shafigat, J.; Beg, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.

Bur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja naja) venom Kunitz-type trypsin inhibitor

A/Reference number: S13846; PMID:1702708

A/Accession: S13846
A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SHA>

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 56.9%; Score 194; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 3.3e-15;
Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 3 RDPFCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTC 57
Db 1 RPFCELPAPAKGICAKHKPAFYNNKDSHCQKFIYGGCGGNANFTTIDECNRTC 55

RESULT 9

TITTOR

basic proteinase inhibitor - loggerhead

C/Species: Caretta caretta (loggerhead)

C/Date: 31-May-1979 #sequence_revision 23-Oct-1981 #ext_change 05-Aug-1994

C/Accession: A01224
R:Kato, I.; Tomimaga, N.

Fed. Proc. 38, 832, 1979

A/Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A/Reference number: A01224

A/Accession: A01224
A/Molecule type: protein

A/Residues: 1-110 <KAT>

C/Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C/Suprafamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;1/Modified site: pyroglutamic acid repeat homology <AIP>

F;8-58,17-41,33-54,67-93,76-97,80-92,86-101/Disulfide bonds: #status predicted

F;18/inhibitory site: Lys (trypsin) #status predicted

Query Match 55.4%; Score 189; DB 1; Length 110;
Best Local Similarity 53.6%; Pred. No. 2.4e-14;
Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 2 DRDPFCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTC 57
Db 3 DRDRIQLPPEQPCGKGRIPRYNNPASKCKNFYIGGCGGNANFTTKECESTC 58

RESULT 10

TIIABK

isoinhibitor K (BPI type) - Roman snail

C/Species: Helix pomatia (Roman snail)

C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #ext_change 05-Aug-1994

C/Accession: A91232; A01225

R:Teichsche, H.; Dietl, T.

Bur. J. Biochem. 58, 439-451, 1975

A/Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequ

A/Reference number: A91232; PMID:76043680; PMID:1183446

A/Accession: A91232
A/Molecule type: protein

A/Residues: 1-58 <TSC>

R:Dietl, T.; Teichsche, H.

Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976

A/Title: Die Disulfidbrücke des Trypsin-Kalikrein-Inhibitors K aus weinbergschnecke

A/Reference number: A91666; PMID:76141310; PMID:3462

A/Contents: annotation; disulfide bonds

C/Comment: This is one of several isoinhibitors of broad specificity that are secreted

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;1/Modified site: pyroglutamic acid (Gln) #status experimental

F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 55.1%; Score 188; DB 1; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.6e-14;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 3 RDPFCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTC 57
Db 3 RSPFCELPAPAKGICAKHKPAFYNNKDSHCQKFIYGGCGGNANFTTIDECNRTC 57

RESULT 11
B59399
short epilon-dendrotoxin H155, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #ext_change 17-May-2002

C/Accession: B59399
R:Sigle, R.; Hackett, M.; Aird, S.D.

Toxicol. 40, 297-308, 2002

A/Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A/Reference number: A59399

A/Accession: B59399
A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <AIR>

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

F;5-55/Disulfide bonds: #status experimental

F;14-38/Disulfide bonds: #status experimental

F;30-51/Disulfide bonds: #status experimental

Query Match 52.5%; Score 179; DB 2; Length 57;
Best Local Similarity 57.7%; Pred. No. 1.7e-13;
Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTC 57
Db 4 FCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKECESTC 55

RESULT 12

TIRPED

venom basic proteinase inhibitor B - black mamba

C/Species: Dendroaspis polylepsis polylepsis (black mamba)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #ext_change 16-Aug-1996

C/Accession: A01215
R:Joubert, F.J.; Strydom, D.J.

Bur. J. Biochem. 87, 191-198, 1978

A/Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis p

A/Reference number: A01215; PMID:78214615; PMID:666688

A/Accession: A01215
A/Molecule type: protein

A/Residues: 1-59 <JOU>

A/Note: this protein inhibits trypsin and binds transition metal ions such as copper a

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C/Keywords: serine proteinase inhibitor; venom
 F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F/7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 52.5%; Score 179; DB 1; Length 59;
 Best Local Similarity 57.7%; Pred. No. 1,7e-13;
 Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRPSPFYNNPDEKCKLEPIYGCCEGNNANFTTKECSTC 57
 DB 6 FCKLPAPGPCASIPAFYNNMAKKCQLPHYGGCKGNANRFTIECKRHAC 57

RESULT 13

Long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps
 C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C/Accession: A59399

R/Sigle: R.; Hackert, M.; Aird, S.D.

Toxinon 40, 297-308, 2002

A/Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A/Reference number: A59399

A/Accession: A59399

A/Status: preliminary

A/Molecule type: protein

A/Residues: 159 <AIR>

A/Note: trypsin inhibitor; K+ channel antagonist

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F/7-57/Disulfide bonds: #status experimental

F/16-40/Disulfide bonds: #status experimental

F/32-53/Disulfide bonds: #status experimental

Query Match 52.5%; Score 179; DB 2; Length 59;
 Best Local Similarity 57.7%; Pred. No. 1,7e-13;
 Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRPSPFYNNPDEKCKLEPIYGCCEGNNANFTTKECSTC 57
 DB 6 FCKLPAPGPCASIPAFYNNMAKKCQLPHYGGCKGNANRFTIECKRHAC 57

RESULT 14

TIRRV2

venom basic proteinase inhibitor II - Russell's viper

C/Species: Viperia russelli (Russell's viper)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C/Accession: A01221

R/Takahashi, H.; Iwanaga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.

J. Biochem. 76, 723-733, 1974

A/Title: Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isolat

A/Reference number: A01221; PMID:75060360; PMID:4436285

A/Accession: A01221

A/Molecule type: protein

A/Residues: 1-60 <TAK>

C/Comment: This inhibitor has activity similar to that of bovine basic protease inhibitd

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 52.2%; Score 178; DB 1; Length 60;
 Best Local Similarity 53.6%; Pred. No. 2.3e-13;
 Matches 30; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 DRPFCFLPADTGPCRVRPSPFYNNPDEKCKLEPIYGCCEGNNANFTTKECSTC 57
 DB 2 DRPFCFLPADTGPCRVRPSPFYNNPDEKCKLEPIYGCCEGNNANFTTKECSTC 57

RESULT 15

TIEPVA

venom basic proteinase inhibitor K - eastern green mamba
 N/Alternate names: dendrotoxin delta-DatX
 C/Species: Dendroaspis angusticeps (eastern green mamba)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
 C/Accession: A91691; C32508; A01213
 R/Joubert, F.J.; Taljaard, N.
 Hoppe-Seyler's Z. Physiol. Chem. 361, 661-674, 1980
 A/Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroas
 A/Reference number: A91691; PMID:81045446; PMID:7429422
 A/Accession: A91691
 A/Molecule type: protein
 A/Residues: 1-57 <QOU>
 R/Benshin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaubein, M.P.
 Mol. Pharmacol. 34, 152-159, 1988
 A/Title: Four polypeptide components of green mamba venom selectively block certain po
 A/Reference number: A93137; PMID:88318591; PMID:2457792
 A/Accession: C32508
 A/Molecule type: protein
 A/Residues: 1-21 <HEN>
 A/Note: the amino acid composition of the inhibitor is identical with that predicted f
 C/Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological
 C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
 C/Keywords: venom
 F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F/5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 49.6%; Score 169; DB 1; Length 57;
 Best Local Similarity 55.8%; Pred. No. 2,2e-12;
 Matches 29; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRPSPFYNNPDEKCKLEPIYGCCEGNNANFTTKECSTC 57
 DB 4 YCKLPVRYGPKCKKIPSPFYNNMAKKCQLPFDYSGCGGNANRFTIECKRHAC 55

Search completed: January 23, 2004, 10:28:10
 Job time: 10.1408 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 5.40141 Seconds
(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179a-2

Sequence: 1 K0RPFCELPADTGPCRVF.....CEGNANNTKECESTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	62.8	65	1VB3_VIPAA	P00992 Vipera ammo
2	204	59.8	62	1P52_ANESU	P10280 anemonta su
3	201	58.9	57	1VB2_NAJNI	P00986 najia nlyea
4	201	58.9	61	1VB1_VIPAA	P00991 vipera ammo
5	198	58.1	57	1VB2_HEMHA	P00985 hemachatus
6	195	57.2	62	1VB2_ERIMA	P24541 eristocophi
7	194	56.9	57	1VB1_NAJNA	P20229 najia najia
8	192	56.3	65	1VB1_BUNFA	P25660 bungarus fa
9	189	55.4	58	1IBP_CARCR	P00993 caretta car
10	188	55.1	110	1ISIK_HELPO	P00994 helix pomat
11	187.5	55.0	55	1CSTI_BOMMO	P81902 bombyx mori
12	179	52.5	58	1ACPI_ANTAF	P81567 anthopleura
13	179	52.5	59	1VB2_DENPO	P00984 dendroaspis
14	179	52.5	230	1TFP2_MOUSE	O35536 mus muscullu
15	178	52.2	60	1VB2_DABRU	P00990 dabola rurs
16	169	49.6	57	1VBK_DEMAN	P00982 dendroaspis
17	169	49.6	302	1TFPI_RAT	O02445 rattus norv
18	169	49.6	306	1TFPI_MOUSE	O54819 mus muscullu
19	168	49.3	57	1VBK_DENPO	P00981 dendroaspis
20	168	49.3	58	1VBK_OPNHA	P82966 ophiophagus
21	168	49.3	304	1TFPI_NACMU	O28864 macaca mula
22	167	49.0	58	1AXP2_ANTAF	P81548 anthopleura
23	165	48.4	57	1SBPI_SABBU	P26228 sarcophaga
24	165	48.4	235	1TFP2_HUMAN	P48307 homo sapien
25	165	48.4	300	1TFPI_RABIT	P19761 oryctolagus
26	163	47.8	252	1SPT2_MOUSE	O9wu03 mus muscullu
27	162.5	47.7	69	1CRPT_BOOMI	P81162 boophilus m
28	161	47.2	252	1SPT2_HUMAN	O43291 homo sapien
29	161	47.2	304	1TFPI_HUMAN	P10666 homo sapien
30	160	46.9	133	1EPTI_HUMAN	O95925 homo sapien
31	160	46.9	3176	1CAB3_HUMAN	P12111 bos sapien
32	156	45.7	100	1BPTI_BOVIN	P00974 bos taurus
33	156	45.7	513	1SPTI_HUMAN	O43278 homo sapien

34	155	45.5	122	1	UPTI_PIG	Q29100 sus scrofa
35	154	45.2	100	1	BPT2_BOVIN	P04815 bos taurus
36	153	44.9	57	1	1VB2_DENPO	P00983 dendroaspis
37	152	44.6	60	1	1BPS_BOVIN	P00975 bos taurus
38	152	44.6	770	1	A4_MOUSE	P12023 m amyloid b
39	150	44.0	76	1	A4_MACMU	P29216 macaca mula
40	150	44.0	751	1	A4_SAISS	O95241 s amyloid b
41	150	44.0	770	1	A4_HUMAN	P05067 h amyloid b
42	150	44.0	770	1	A4_MACFA	P53601 m amyloid b
43	150	44.0	770	1	A4_PIG	P79307 s amyloid b
44	150	44.0	770	1	A4_RAT	P08592 r amyloid b
45	149	43.7	55	1	1SH1_STOHE	P31713 scolichactis

ALIGNMENTS

RESULT 1	1VB3_VIPAA	STANDARD;	PRT;	65 AA.
ID	1VB3_VIPAA	STANDARD;	PRT;	65 AA.
AC	P00992;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Viperidae; Viperinae; Vipera.			
ON	NCBI_TaxID=8705;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RA	Ritonja A., Meloun B., Gubensek F.;			
RT	"The primary structure of Vipera ammodytes venom chymotrypsin inhibitor."			
RL	Biochim. Biophys. Acta 746:138-145(1983).			
CC	-1- FUNCTION: This protein inhibits chymotrypsin.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01223; TIVVC.			
DR	HSSP; P31713; ISHP.			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	ProDom; PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KUF; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Serine protease inhibitor.			
FT	DISULFID 7 57			
FT	DISULFID 16 40			
FT	DISULFID 32 53			
FT	ACT_SITE 17 18			
FT	SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;			
FT	REACTIVE_BOND (BY SIMILARITY).			
QY	1 K0RPFCELPADTGPCRVFPPSYNPDEKCLEFTYGGCEGNANNTKECESTCA 59			
Db	1 R0RPFCELPADTGPCRVFPPSYNPDEKCLEFTYGGCEGNANNTKECESTCA 59			
Query Match	Best Local Similarity	62.8%;	Score 214;	DB 1; Length 65;
Matches	37; Conservative	3;	Mismatches	19; Indels
			Gaps	0;
RESULT 2	1P52_ANESU	STANDARD;	PRT;	62 AA.
ID	1P52_ANESU	STANDARD;	PRT;	62 AA.
AC	P10280;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Protease inhibitor 5 II (SAS II).			
OS	Anemonta sulcata (Snake-locks sea anemone).			

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OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymathea; Actiniidae; Anemona.
OX NCBI_Taxid=6108;
RN SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
RT Anemona sulcata."
RL Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
RT from the sea anemone Metridium senile."
RL Naturwissenschaften 74:395-396(1987).
CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P31713; 1SHP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT ACT SITE 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 13 13 P -> G.
FT VARIANT 16 16 R -> R.
FT VARIANT 17 17 A -> G.
FT VARIANT 17 17 S -> L.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 59.8%; Score 204; DB 1; Length 62;
Best Local Similarity 66.7%; Pred. No. 4.8e-18;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 7 CELPADGPRCPVRPSPFYNDKKCLEFTYGGCGGNANPITKECESTC 57
DB 5 CELPKVGPCKARPRFYTNSSKRCCKFTYGGCGGNANPHTLSECKVC 55

RESULT 3
ID IVB2_NAJNI STANDARD; PRT; 57 AA.
AC P00986;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja naja (Cape cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Naja.
OX NCBI_Taxid=6655;
RN [1]
RP SEQUENCE.
RA TISSUE=Venom;
RX MEDLINE=76237547; PubMed=950337;
RA Hokama Y., Iwanaga S., Tateuchi T., Suzuki T.;
RT "Snake venom proteinase inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
RT (Ringal's cobra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them."
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
CC that of bovine basic protease inhibitor.
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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01217; TINVJC.
DR HSSP; P00981; IDPTC.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6466 MW; 7CA6923D0A0287D1 CRC64;

Query Match 58.9%; Score 201; DB 1; Length 57;
Best Local Similarity 63.6%; Pred. No. 1e-17;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 3 RPDPCGLPADTGPCVRPSPFYNDKKCLEFTYGGCGGNANPITKECESTC 57
DB 1 RPRCELPATGCLCKARIRSFHYRAAQCCLEFTYGGCGGNANPRTIDECRTG 55

RESULT 4
ID IVB1_VIPAA STANDARD; PRT; 61 AA.
AC P00991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor I (Venom trypsin inhibitor I).
OS Viperina amodytes amodytes (Western sand viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Viperina.
OX NCBI_Taxid=8705;
RN [1]
RP SEQUENCE.
RA TISSUE=Venom;
RX MEDLINE=84053385; PubMed=6639951;
RA Ritonja A., Meloun B., Gubensek F.;
RT "The primary structure of Viperina amodytes venom trypsin inhibitor
RT I."
RL Biochim. Biophys. Acta 748:429-435(1983).
CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01222; TIVT1.
DR HSSP; P31713; 1SHP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
SQ SEQUENCE 61 AA; 6865 MW; FC8285F579FE3795 CRC64;

Query Match 58.9%; Score 201; DB 1; Length 61;
Best Local Similarity 57.6%; Pred. No. 1.1e-17;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 KDPDCELPADTGPCVRPSPFYNDKKCLEFTYGGCGGNANPITKECESTCA 59
DB 1 QDHPKFCPLPADGPKCKAHIPRFYDASNSCKNKFYGGCGGNANPFTWDECRGTGA 59
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RESULT 5
 ID IVB2_HEMMA STANDARD; PRT; 57 AA.
 AC P00955;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Ringhals) (Sepedon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Hemachatus.
 OC NCB1_TaxID=8626;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokama Y., Iwanaga S., Tateuchi T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Ringhals cobra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them.";
 RL J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC -1- bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC PIR; A01216; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7F2A CRC64;
 Query Match 58.1%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 2,3e-17;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 3 RPDCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTC 57
 DB 1 RPDCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTC 55
 RESULT 6
 ID IVBT_ERIMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis machaoni (Leaf-nosed viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Eristocophis.
 OC NCB1_TaxID=8702;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 RT from leaf-nosed viper venom.";
 RL FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S19327; S19327.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 2 52 BY SIMILARITY.
 FT DISULFID 11 35 BY SIMILARITY.
 FT DISULFID 27 48 BY SIMILARITY.
 FT ACT_SITE 12 13 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;
 Query Match 57.2%; Score 195; DB 1; Length 62;
 Best Local Similarity 61.1%; Pred. No. 5.8e-17;
 Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;
 QY 6 FCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTCA 59
 DB 1 FCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTCA 54
 RESULT 7
 ID IVBT_NAJNA STANDARD; PRT; 57 AA.
 AC P20229;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OC NCB1_TaxID=35670;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91099304; PubMed=1702708;
 RA Shaqfat J., Beg O.U., Yin S.-U., Zaidi Z.H., Joernvall H.;
 RT "Primary structure and functional properties of cobra (Naja naja
 RT naja) venom Kunitz-type trypsin inhibitor.";
 RL Eur. J. Biochem. 194:337-341(1990).
 CC -1- FUNCTION: This protein inhibits trypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC PIR; S13846; S13846.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6371 MW; AABFD72949ADC12A CRC64;
 Query Match 56.9%; Score 194; DB 1; Length 57;
 Best Local Similarity 60.0%; Pred. No. 7e-17;
 Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 3 RPDCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTC 57
 DB 1 RPDCELPADTGPCVRRPSPFYNPDEKCKLEFIYGGCGGNANFETKECESTC 55

DB 1 REPFCFLPAKGLCKAKHKAPEFYNNKDSHRCQKEFYGGCGGNANPRTIDECNRTC 55

RESULT 8

1VB1_BUNFA STANDARD; PRT; 65 AA.

AC P25660;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Venom basic protease inhibitors IX and VIIIB.

OS Bungarus fasciatus (Banded Krait).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Elapidae; Bungarinae; Bungarus.

OX NCBI_Taxid=8613;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=83160048; PubMed=6832893;

RA Liu C.-S., Wu T.-C., Lo T.-B.;

RT "Complete amino acid sequences of two protease inhibitors in the venom of Bungarus fasciatus.";

RL Int. J. Pept. Protein Res. 21:209-215(1983).

CC -1- FUNCTION: Inhibitor of chymotrypsin.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR HSP; P00980; IDTX.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

DR Serine protease inhibitor.

FT DISULFID 7 57 BY SIMILARITY.

FT DISULFID 16 40 BY SIMILARITY.

FT DISULFID 32 53 BY SIMILARITY.

FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).

FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).

FT SEQUENCE 65 AA; 7294 MW; BA340749E194DB51 CRC64;

SO QUERY MATCH

Best Local Similarity 56.3%; Score 192; DB 1; Length 65;

Matches 34; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 KRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGNANPRTKECESTCA 59

DB 1 KRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGNANPRTKECESTCA 59

RESULT 9

1BP_CARCR STANDARD; PRT; 110 AA.

AC P00993;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chelonanthin (Basic protease inhibitor) (RTP1).

OS Caretta caretta (Loggerhead).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Testudines; Cryptodira; Chelonioidea; Cheloniidae; Caretta.

OX NCBI_Taxid=8467;

RN [1]

RP SEQUENCE.

RC TISSUE=Egg white;

RA Kato I., Tomimaga N.;

RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tandem domains -- one Kunitz -- one of a new family.";

CC Fed. Proc. 38:832-832(1979).

CC -1- FUNCTION: THE FIRST DOMAIN INHIBITS TRYPSIN; THE SECOND ONE INHIBITS SUBTILISIN.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -1- SIMILARITY: Contains 1 WAP-type domain.

CC -1- CAUTION: AS THE PAPER ONLY INDICATES THE SPECIES AS "RED SEA TURTLE", THE SPECIES INDICATED HERE IS THEREFORE AN INFERENCE.

DR PIR; A01224; TITROR.

DR HSP; P00974; 6PTI.

DR InterPro; IPR002223; Kunitz_BPTI.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR Pfam; PF00095; Wap; 1.

DR PRINTS; PR00009; 4DISULPHCORE.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

DR Serine protease inhibitor; Pyroglutamate carboxylic acid. BPTI/KUNITZ INHIBITOR.

FT DOMAIN 8 58 WAP.

FT MOD_RES 63 105 PYROGLUTAMATE CARBOXYLIC ACID.

FT DISULFID 8 58 BY SIMILARITY.

FT DISULFID 17 41 BY SIMILARITY.

FT DISULFID 33 54 BY SIMILARITY.

FT DISULFID 67 92 BY SIMILARITY.

FT DISULFID 76 97 BY SIMILARITY.

FT DISULFID 80 93 BY SIMILARITY.

FT DISULFID 86 101 BY SIMILARITY.

FT ACT SITE 18 19 REACTIVE BOND (TRYPSIN).

FT SEQUENCE 110 AA; 11916 MW; 269436243813418E CRC64;

SO QUERY MATCH

Best Local Similarity 55.4%; Score 189; DB 1; Length 110;

Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 2 DRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGNANPRTKECESTC 57

DB 3 DRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGNANPRTKECESTC 57

RESULT 10

ISIK_HELPO STANDARD; PRT; 58 AA.

AC P00954;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Helix pomatia (Roman snail) (Edible snail).

OS Helix pomatia (Roman snail) (Edible snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Stigmurethra; Helicoidea; Helicidae; Helix.

OX NCBI_Taxid=6536;

RN [1]

RP SEQUENCE.

RX MEDLINE=76043680; PubMed=1183446;

RA "The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequence determination by automated Edman degradation and mass-spectral identification of the phenylthiohydantoina.";

RT Eur. J. Biochem. 58:439-451(1975).

RL [2]

RP DISULFIDE BONDS.

RX MEDLINE=76141310; PubMed=3462;

RA Dietl T., Tschesche H.;

RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from snails (Helix pomatia). Thermal inactivation and proteolysis by thermolysin.";

RT Hoppe-Seyler's Z. Physiol. Chem. 357:139-145(1976).

CC -1- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR PIR, A91232, TTHAK.
 DR HSP; P00974; 1BP1.
 DR InterPro; IPR002223; Kunitz_BPT1.
 DR Pfam; PF00014; Kunitz_BPT1; 1.
 DR ProDom; PD000222; Kunitz_BPT1; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPT1_KUNITZ_2; 1.
 KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT DISULFID 7 57 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17 18
 SQ SEQUENCE 58 AA; 6451 MW; 6796586C48453B7 CRC64;
 REACTIVE BOND (BY SIMILARITY).
 Query Match 55.1%; Score 188; DB 1; Length 58;
 Best Local Similarity 52.7%; Pred. No. 3.6e-16;
 Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 3 RPDCELPADTGPCRVPRFSPFYNNPDEKCKLEFIYGCCEGNANNFITKECESTC 57
 DB 3 RSPFCULPPIATGCGKASFRQYINSSKSGCGQPIYGGCRANQNRFTTQCCQGV 57
 RESULT 11
 CSTI_BOMMO STANDARD; PRT; 55 AA.
 ID CSTI_BOMMO
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 [1]
 RP SEQUENCE. AND CHARACTERIZATION.
 RC STRAIN=Asahi;
 RX MEDLINE=9115431; PubMed=9914483;
 RA Kuritoka A., Yamazaki M., Hirano H.;
 RT "Primary structure and possible functions of a trypsin inhibitor of Bombyx mori."
 RL Eur. J. Biochem. 259:120-126(1999).
 CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin activity by forming a low-dissociation complex with trypsin. May play an important part in regulating proteolytic activity in the silk gland or protecting silk proteins from degradation during histolysis.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk gland.
 CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the middle silk glands during the final stage of larval growth with highest expression before the onset of spinning.
 CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
 CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
 CC -1- SIMILARITY: BELONGS TO THE BPT1/KUNITZ FAMILY OF INHIBITORS.
 DR HSP; P11713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPT1.
 DR Pfam; PF00014; Kunitz_BPT1; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPT1; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPT1_KUNITZ_2; 1.
 KW Developmental protein; Serine protease inhibitor.
 FT DISULFID 4 54
 FT DISULFID 13 37 BY SIMILARITY.
 FT DISULFID 29 50 BY SIMILARITY.
 FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY

FT SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2BB6E59 CRC64;
 SIMILARITY).
 Query Match 55.0%; Score 187.5; DB 1; Length 55;
 Best Local Similarity 61.1%; Pred. No. 4.1e-16;
 Matches 33; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
 QY 4 PDCCELPADTGPCRVPRFSPFYNNPDEKCKLEFIYGCCEGNANNFITKECESTC 57
 DB 2 PD-CLIPKPGPKGSPRYAVDSSEKCYEPIYGCCEGNANNFETIECCAC 54
 RESULT 12
 AXPI_ANTAF STANDARD; PRT; 58 AA.
 ID AXPI_ANTAF
 AC P8157;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kunitz-type proteinase inhibitor AXPI-1.
 OS Anthopleura aff. xanthogrammica (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nymanthea; Actiniidae; Anthopleura.
 OX NCBI_TaxID=152178;
 [1]
 RP SEQUENCE.
 RX MEDLINE=98103405; PubMed=9440231;
 RA Minagawa S., Iehida M., Shimakura K., Nagashima Y., Shiom K.;
 RT "Isolation and amino acid sequences of two Kunitz-type protease inhibitors from the sea anemone Anthopleura aff. xanthogrammica."
 RL Comp. Biochem. Physiol. 118B:381-386(1997).
 CC -1- FUNCTION: SPECIFIC FOR SERINE PROTEASES, ESPECIALLY TRYPSIN. ALSO WEAK INHIBITION AGAINST ALPHA-CHYMOTRYPSIN, ELASINASE AND SOME METALLOPROTEASES.
 CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
 DR HSP; P11713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPT1.
 DR Pfam; PF00014; Kunitz_BPT1; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPT1; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPT1_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40 BY SIMILARITY.
 FT DISULFID 32 53 BY SIMILARITY.
 FT ACT_SITE 17 18 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 58 AA; 6341 MW; DA7216A535EA7CC CRC64;
 Query Match 52.5%; Score 179; DB 1; Length 58;
 Best Local Similarity 58.8%; Pred. No. 4.6e-15;
 Matches 30; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
 QY 7 CELPADTGPCRVPRFSPFYNNPDEKCKLEFIYGCCEGNANNFITKECESTC 57
 DB 7 CLLPKPGPKGSPRYAVPRFYNSDSKCBGFTYGCCEGNANNFITKECKNAC 57
 RESULT 13
 IYBE_DENPO STANDARD; PRT; 59 AA.
 ID IYBE_DENPO
 AC P00964;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor E (Dendrotoxin E).
 OS Dendroaspis polylepis polylepis (Black mamba).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubridae; Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8620;
 [1]

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RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=78214615; PubMed=668688;
RA Joubert F.J., Strydom D.J.;
RT "Snake venoms. The amino-acid sequence of trypsin inhibitor E of
RT Dendroaspis polylepsis polylepsis (Black Mamba) venom.";
RL Eur. J. Biochem. 87:191-198(1978).
CC -1- FUNCTION: This protein inhibits trypsin and binds transition metal
CC ions such as copper and cobalt.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01215; TIEPED.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI_1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 59 AA; 6620 MW; E87BPECC0090276 CRC64;

Query Match 52.5% Score 179; DB 1; Length 59;
Best Local Similarity 57.7%; Pred. No. 4.7e-15;
Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 6 FCELPADTGRCVRPSPFYNPDEKCKLEPIYGCCEGNANFTKEBCESTC 57
Db 6 FCKLPAGPCFKASIPATYVMAKKQLFHYGCKGNANFTSEKCRHAC 57

RESULT 14
TFP2 MOUSE STANDARD; PRT; 230 AA.
AC 035536;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
GN TFP12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Placenta;
RX MEDLINE=97101108; PubMed=8945635;
RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,
RA Itoh H., Hori T., Aoki I., Miugai K., Miyazaki K.;
RT "Cloning of the cDNA encoding mouse pps/TFPI-2 and mapping of the gene
RT to chromosome 6.";
RL DNA Cell Biol. 15:947-954(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=20132652; PubMed=10669168;
RA Karama Y., Kamei S., Kujiper J.L., Foster D.C., Klatel W.;
RT "Nucleotide sequence of the gene encoding murine tissue factor pathway
RT inhibitor-2.";
RL Thromb. Haemost. 83:141-147(2000).
CC -1- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
CC WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA. ALSO EXPRESSED
CC IN LIVER AND KIDNEY.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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CC -----
DR EMBL; D50586; BAA22585.1; -
DR EMBL; AF180353; AAP40412.1; -.
DR HSSP; P12111; IKNV.
DR MGD; MG1.108543; TPI2.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI_2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Signal;
KW Blood coagulation.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 230 TISSUE FACTOR PATHWAY INHIBITOR 2.
FT DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 96 146 BPTI/KUNITZ INHIBITOR 2.
FT DOMAIN 156 206 BPTI/KUNITZ INHIBITOR 3.
FT ACT SITE 46 47 REACTIVE BOND (BY SIMILARITY).
FT ACT SITE 106 107 REACTIVE BOND (BY SIMILARITY).
FT ACT SITE 166 167 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 36 86 BY SIMILARITY.
FT DISULFID 45 69 BY SIMILARITY.
FT DISULFID 61 82 BY SIMILARITY.
FT DISULFID 96 146 BY SIMILARITY.
FT DISULFID 105 129 BY SIMILARITY.
FT DISULFID 121 142 BY SIMILARITY.
FT DISULFID 156 206 BY SIMILARITY.
FT DISULFID 165 189 BY SIMILARITY.
FT DISULFID 181 202 BY SIMILARITY.
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 230 AA; 26137 MW; 57BAD2B36521C7B CRC64;

Query Match 52.5% Score 179; DB 1; Length 230;
Best Local Similarity 50.9%; Pred. No. 1.9e-14;
Matches 28; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 5 DCELPADTGRCVRPSPFYNPDEKCKLEPIYGCCEGNANFTKEBCESTCA 59
Db 34 EICLPFDAGPCQALIPKRYVDROQKCRFRNYGGLGNANFHSRDLCOOTCS 88

RESULT 15
IYB2 DABRU STANDARD; PRT; 60 AA.
ID IYB2 DABRU
AC P00930;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II (RVV-II).
DE Daboia russellii siamensis (Siamese Russell's viper) (Vipera russelli
DE siamensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Daboia.
OX NCBI_TaxID=8708;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=75060360; PubMed=4436285;
RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
RT "Snake venom proteinase inhibitors. II. Chemical structure of
RT inhibitor II isolated from the venom of Russell's viper (Vipera
RT russelli).";

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RL J. Biochem. 76:721-733(1974).
 CC -1- FUNCTION: This inhibitor has activity similar to bovine basic
 CC protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HESP, P10646; IADP.
 DR InterPro, IPR002223; Kunitz_BPTI.
 DR Pfam, PF00014; Kunitz_BPTI, 1.
 DR ProDom, PD000222; Kunitz_BPTI, 1.
 DR SMART, SM00131; KU, 1.
 DR PROSITE, PS00260; BPTI_KUNITZ_1, 1.
 DR PROSITE, PS50279; BPTI_KUNITZ_2, 1.
 KM Serine protease inhibitor.
 FT DISULFID 7 57
 FT FT 6 40
 FT DISULFID 32 18
 FT ACT SITE 17 53
 SO SEQUENCE 60 AA; 6650 MW; 5A7DCE954CE6A2 CRC64;

Query Match	52.2%	Score 178	DB 1	length 60
Best Local Similarity	53.6%	Pred. No. 6.2e-15		
Matches 30, Conservative		5, Mismatches 21,	Indels 0,	Gaps 0,

Qy 2 DRPFCLEPADTGPGRVRFPSFYNNPEKKCLEFIYGGEGGNANNPITKEECSTC 57
||| : ||| : ||| ||| ||| : ||| |||
Db 2 DRPTFCNLAPESGRGRHLRRIYNNLESNKKRVFFYGGCGGNANNPETRDECRETC 57
||| : ||| : ||| ||| ||| : ||| |||

Search completed: January 23, 2004, 10:25:14
Job time : 6.40141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 22.2289 seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179A-8
Perfect score: 342
Sequence: 1 KDHPKFCLEPAETGSCRGKV.....CGGNANPKTIEGKSTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	96.5	83	13	Q90W98 pseudonaja
2	256	74.9	83	13	Q90W99 pseudonaja
3	225	65.8	83	13	Q90W91 pseudonaja
4	217	63.5	83	13	Q90W90 pseudonaja
5	206	60.2	83	13	Q90W96 pseudonaja
6	201	58.8	83	13	Q90W97 pseudonaja
7	201	58.8	88	13	Q90W93 pseudonaja
8	191	55.8	88	13	Q8AY42 pseudonaja
9	187	54.7	88	13	Q8AY41 pseudonaja
10	187	54.7	142	5	Q8WP12 boophilus m
11	184	53.8	142	5	Q8WP13 boophilus m
12	183	53.5	59	5	Q8TW68 anemonia su
13	178	52.0	79	13	Q91351 dendroaspis
14	173	50.6	58	5	Q91W60 anemonia su
15	172	50.3	76	5	Q8T719 bombyx mori
16	168	49.1	267	6	Q8MI34 ovis aries

17	168	49.1	506	6	Q8MI33 ovis aries
18	164	48.0	82	5	Q8WVB4 ixodes scap
19	162	47.4	58	5	Q9TW69 anemonia su
20	158	46.2	287	13	Q93424 cyprinus ca
21	157	45.9	235	11	Q8C180 mus musculus
22	157	45.9	235	11	Q8BSB7 canis fam1
23	156	45.6	396	6	Q28874 canis fam1
24	154	45.0	80	5	Q8T367 araneus ven
25	154	45.0	1487	5	Q8WPV5 caenorhabdi
26	154	45.0	1558	5	Q8T710 caenorhabdi
27	154	45.0	2167	5	Q76840 caenorhabdi
28	153	44.7	984	5	Q9GON2 calliactis
29	153	44.7	984	5	Q9GON1 calliactis
30	152	44.4	249	5	Q16701 caenorhabdi
31	151	44.2	277	13	Q8AY61 ancylostoma
32	151	44.2	759	5	Q8T791 ancylostoma
33	150	43.9	167	4	Q8RE89 homo sapien
34	150	43.9	224	4	Q8NAK6 homo sapien
35	148	43.3	183	6	Q9N0X5 bos taurus
36	148	43.3	230	11	Q8CFP9 rattus norv
37	146.5	42.8	113	5	Q9V508 drosophila
38	146	42.7	154	6	Q9N0X3 ovis aries
39	146	42.7	576	4	Q8REU8 homo sapien
40	146	42.7	2225	5	Q45881 caenorhabdi
41	145	42.4	169	6	Q9N0X7 bos taurus
42	145	42.4	3198	5	Q9U8G8 manduca sex
43	144	42.1	819	5	Q19305 caenorhabdi
44	143	41.8	507	11	Q9D3K4 mus musculus
45	143	41.8	507	11	Q9J004 mus musculus

ALIGNMENTS

RESULT 1
Q90W98 PRELIMINARY; PRT; 83 AA.
AC Q90W98;
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Textillin.
OS Pseudonaja textilis textilis.
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masel P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasma inhibitors from the Australian Brown Snake Pseudonaja
textilis textilis."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Filipovich I.V., Sorokina I.N., Masel P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402327; AAK95522.1; -;
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PDOM00222; Kunitz_BPTI_1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 8983 MW; 3F28548146B8A2B CRC64;
Query Match 96.5%; Score 330; DB 13; Length 83;
Best Local Similarity 96.6%; Pred. No. 1.2e-33;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 DB 25 KDHPKCELPADTGCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 2

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophiliinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Pliipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Gaffney P.J., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Pliipovich I.V., Gaffney P.J., Lavin M.F.,
 RA Whitaker A.N., Kunitz BPTI; 1.
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95521.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9158 MW; 366E82487ACPB61 CRC64;

Query Match 74.9%; Score 256; DB 13; Length 83;
 Best Local Similarity 71.2%; Pred. No. 2e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 DB 25 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 3

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophiliinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Pliipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
 RA Pliipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95519.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9173 MW; 2045850657014221 CRC64;

Query Match 65.8%; Score 225; DB 13; Length 83;
 Best Local Similarity 67.8%; Pred. No. 1.5e-20;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 DB 25 KDHPKCELPADTGCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 4

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophiliinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Pliipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Pliipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RA Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95520.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9179 MW; 67589AD27175930 CRC64;

Query Match 63.5%; Score 217; DB 13; Length 83;
 Best Local Similarity 64.4%; Pred. No. 1.5e-19;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 DB 25 KDHPKCELPADTGCCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 5

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)

Db 30 KDRPFCNVPPGRCNANVAFYNNPRLKCIFFTYGGCGGNANFKSGEGRAC 86

RESULT 9
Q8AY41 PRELIMINARY; PRT; 88 AA.

AC Q8AY41; 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
OS Kunitz inhibitor C (Fragment).
OC Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC NCB1_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY057888; AAL30070.1; -
FT NON TER 1 1
SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;

Query Match 54.7%; Score 187; DB 13; Length 88; V
Best Local Similarity 58.6%; Pred. No. 8.7e-16;
Matches 34; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 KDHPFCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTCA 58
Db 30 KDRPFCNVPPGRCNANVAFYNNPRLKCIFFTYGGCGGNANFKTIDECQRTCA 87

RESULT 10
Q8WP12 PRELIMINARY; PRT; 142 AA.

DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Boophilin precursor.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCB1_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
RT characterization, cloning and three-dimensional model of its complex
RT with thrombin."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Pereira P.J.; Universidade do Porto, Oporto, Portugal.
RL EMBL; AJ304447; CAC82583.1; -
DR InterPro; IPR002223; Kunitz_BPT1.
DR Pfam; PF00014; Kunitz_BPT1_2.
DR PRINTS; PR00759; BasicPRASE.
DR PRODOM; PD000222; Kunitz_BPT1_2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 2.
DR PROSITE; PS0279; BPT1_KUNITZ_2; 2.
KW Protease inhibitor; Serine protease inhibitor; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 142 BOOPHILIN, ISOFORM H2.
SQ SEQUENCE 142 AA; 15538 MW; 88BP0008BD42010 CRC64;

Query Match 54.7%; Score 187; DB 5; Length 142;
Best Local Similarity 57.4%; Pred. No. 1.4e-15;
Matches 31; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTCA 59
Db 20 FCRLPADGICKALIPRFYNTGKCMFSGCGGNENFETIEGCKACGA 73

RESULT 11
Q8WP13 PRELIMINARY; PRT; 142 AA.

DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
OS Boophilin precursor (Cattle tick).
OC Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCB1_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
RA Mentale R., Huber R., Bode W., Fuentes-Prior P.;
RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
RT characterization, cloning and three-dimensional model of its complex
RT with thrombin."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Pereira P.J.; Universidade do Porto, Oporto, Portugal.
RL EMBL; AJ304446; CAC82582.1; -
DR InterPro; IPR002223; Kunitz_BPT1.
DR Pfam; PF00014; Kunitz_BPT1_2.
DR PRODOM; PD000222; Kunitz_BPT1_2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 2.
DR PROSITE; PS0279; BPT1_KUNITZ_2; 2.
KW Protease inhibitor; Serine protease inhibitor; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 142 BOOPHILIN, ISOFORM G2.
SQ SEQUENCE 142 AA; 15555 MW; EA6EC742D3159705 CRC64;

Query Match 53.8%; Score 184; DB 5; Length 142;
Best Local Similarity 55.6%; Pred. No. 3.4e-15;
Matches 30; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTCA 59
Db 20 FCRLPADGICKALIPRFYNTGKCMFSGCGGNENFETIEGCKACGA 73

RESULT 12

Q9TWF8 PRELIMINARY; PRT; 59 AA.

DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE KALICLUDINE 3, ASK3.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoontharia; Actinaria;
OC Nyantheae; Actinidae; Anemonia.
OX NCB1_TaxID=6108;
RN [1]
RP SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemane E., Moynier D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicludine and kalieptine. Two different classes of sea anemone
RT toxins for voltage sensitive K⁺ channels."

RL J. Biol. Chem. 270:25121-25126(1995).
 DR HSP; P31713; 1SH.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394DA5 CRC64;

Query Match 53.5%; Score 183; DB 5; Length 59;
 Best Local Similarity 58.8%; Pred. No. 1.8e-15;
 Matches 30; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 7 CELPAETGSCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57
 Db 5 CELPKVGRCRAPPRRYNNLSRRCEKFIYGGCGGANNFKTIEGKVC 55

RESULT 13

ID Q91351 PRELIMINARY; PRT; 79 AA.
 AC Q91351;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Dendrotoxin K (Fragment).
 GN DENDROTOXIN K, DTXK.
 OS Dendroaspis polylepsis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 OC NCBI_TaxID=8624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277850; PubMed=8504088;
 RA Smith L.A., Lafaye P.J., Lapenotiere H.P., Spain T., Dolly J.O.;
 RT "Cloning and functional expression of dendrotoxin K from black mamba,
 a K⁺ channel blocker."
 RL Biochemistry 32:5692-5697(1993).
 DR EMBL; S61866; AAB26898.1; -
 DR HSP; P00981; DTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 FT NON TER 1 1
 SQ SEQUENCE 79 AA; 8851 MW; DCDPB9AFA07D7D46 CRC64;

Query Match 52.0%; Score 178; DB 13; Length 79;
 Best Local Similarity 58.5%; Pred. No. 1e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 5 KFCLEPATGSCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57
 Db 25 KYCCLPRLRGCKRKIPRYKMKAKCCLPFDYSGCGGANNFKTIEGKRTC 77

RESULT 14

ID Q9TWGO PRELIMINARY; PRT; 58 AA.
 AC Q9TWGO;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE KALICUDINE 1, ASKCI.
 OS Anemonia sulcata (Snake-locks sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Myantheae; Actinidae; Anemonia.
 OC NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE.

FX MEDLINE=96027617; PubMed=7559645;
 RA Beres L., Lazdunski M.,
 RA Schweltz H., Bryhn T., Guillemane E., Moinier D., Lancelin J.M.,
 RT "Kalicudines and kalipectine. Two different classes of sea anemone
 toxins for voltage sensitive K⁺ channels."
 RL J. Biol. Chem. 270:25121-25126(1995).

DR HSP; P10646; 1MDZ.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 58 AA; 6691 MW; 253B068896B4BD0D CRC64;

Query Match 50.6%; Score 173; DB 5; Length 58;
 Best Local Similarity 54.7%; Pred. No. 3.2e-14;
 Matches 29; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 5 KFCLEPATGSCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57
 Db 3 KDCLEPMDVGRCRASHRRYNNLSRRCEKFIYGGCGGANNFKTIEGKVC 55

RESULT 15

ID Q8T7L9 PRELIMINARY; PRT; 76 AA.
 AC Q8T7L9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Kazal-type serine proteinase inhibitor 1.
 GN SP11.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OC NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21873253; PubMed=11881808;
 RA Nirmala X., Mita K., Vanisree V., Zurovec M., Sehna F.;
 RT "Identification of four small molecular mass proteins in the silk of
 Bombyx mori."
 RL Insect Mol. Biol. 10:437-445(2001).
 DR EMBL; AF352583; AAL83944.1; -
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 FT NON TER 1 1
 SQ SEQUENCE 76 AA; 8445 MW; AA3F97D37353A3B CRC64;

Query Match 50.3%; Score 172; DB 5; Length 76;
 Best Local Similarity 54.9%; Pred. No. 5.6e-14;
 Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 7 CELPAETGSCKGNVPRFYNNADHQCCKFYGGCGGANNFKTIEGKSTC 57
 Db 25 CLVIRKTPCKGSPRAYVDSBDKCVFIYGGCGGANNFKTIEGCAAC 75

Search completed: January 23, 2004, 10:27:16
 Job time : 23.2289 secs

